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SOR REPRESENTATION OF STREET OF STRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               258 KWNYIYDKLSVHVTALTHLPTFSIPGTLESGHPRNLTCSVPWACBOGTPPTITWMCASVS 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187 SQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVISIS 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 RDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----PPONLTMTVPQGDGTASTTLRNGSALSVLEGQSLHLVCAVDSNPPARLSWTWGS 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             420 ITLSPSQSSNLGVLELPRVHVKDEGEFTCRAQNPLGSQHISLSLSLQNEYIGKMRPISGV 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLGAVGGAGATALVFLSFCIIFVVV---RSCRKKSARPAVGVGDTGMEDTNAVRGSASQG 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLAOKRNOKATPNSPRTPLPPGAPSPESKKNOKKOYOLPSFPEPKSSTOAPESQESQEEL 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 TTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRVERGSYV
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                                                                                                                                                                                                                                                   Ig-like lectin-like
HSSP, Q9Y286; 1078.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
Pfam; PF00047; ig; 4.
SMART; W000408; IGc2; 1.
SMART; W000408; IG_LIKE; 3.
Cell adhesion; Glycoprotein; Immunoglobulin domain; Lectin; Repeat; S1gnal; Transmembrane.
SIGNAL
21 597 Sialic acid binding Ig-like lectin-like.
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.larity 41.4%; Pred. No. 1.4e-53;
Conservative 70; Mismatches 164; Indels
                                                                                                                                                                                                                                                                                                                                             Cyconicanic (Potential).

Ig-like V-type 1.

Ig-like V-type 2.

Ig-like C2-type 1.

Ig-like C2-type 2.

Ig-like C2-type 2.

ITIM motif.

SLAM-LIKE MOTIF.

By similarity.

N-linked (GlCNAC. ..) (P.
N-linked (G
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N-linked
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es 212; Conserv
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CARBOHYD
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     SOUNTERPRESENTATIONS
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STRAIN=CZECH IN.

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STRAIN=CZECH IN.

C STRAIN=CZECH IN.

C STRAIN=CZECH IN.

C EXPression driven metastatized to lung. MMTV-LTR/Wnt1 model.

EXPRESSION driven by an MMTV-LTR enhancer.

C EXPRESSION driven by an MMTV-LTR enhancer.

C STRAIN=CZECH IN.

C EXPRESSION DRIVEN BY AN GROUSE L.H., Derge J.G.,

C Strausberg R.L., Felngold E.A., Grouse L.H., Derge J.G.,

A Riausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buccow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hashe F.,

Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.B., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Marzy, Sodergen E.J., Lu X., Glbbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz D., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalsku U., Smailus D.E., Schnerch A., Schein J.E.,
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                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Makaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCB_TaxID=10090;
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Expression driven by an MMTV-LTR enhancer.;
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EMBL, BC023280; AAH3280.1; -.
EMBL, BC004872; F:receptor activity; IDA.
GO:00005057; F:receptor signaling protein activity; IPI.
GO: GO:0007155; F:receptor signaling
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Interpro; IPR003599; Ig.
Interpro; IPR003599; Ig.
Interpro; IPR003506; Ig_MHC.
Pfam; PF000409; Ig_2MHC.
SWART; SW00409; IGC2; 1.
PR0371TE; PS50835; IG LIKE; 2.
PR0371TE; PS50835; IG LIKE; 2.
PR0371TE; RS00290; IG MHC; UNKNOWN 1.
SEQUENCE 468 AA; 51987 MW; 26A0FF74D3CA4ACF CRC64;
                                                                                                         Last sequence update)
Last annotation update)
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                                                                           Created)
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PRELIMINARY;
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                                                                                                                                                                                                                       Name=Siglecl1;
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05-JUL-2004
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Q6PJ50;
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233 RVAYAPRDLVISISRDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVT
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                                  238 NVSYAPK---
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SEQUENCE FROM N.A.
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Submitted (A
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                                 113 ESQYFFRVERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEE 172
                                                                                                                                                                                                                                                                                                               353 HYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTE----TPRPRFSRHST 408
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                                                       CPPPSFSWTGAALSSQGTXPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRL
                                                                                                                                      180 TAPPIPSWIGTSVSFLSTNTIGS -- SVLTITPQPQDHGTNLTCQVTLPGTDVSTRMTIRL
                                                                                                                                                                                                          238 NVSYAPK-------NLTVTIYQGADSVSTILKNGSSLPISEGQSLRLICST
                                                                                                                                                                                                                                                                                                                                     342 QSSATL--SEMMGTFVGSGVTALLFLSVCILLLAVRSYRRPARPAVVAPHP-----
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                                                                                                                                                                         RVAYAPRDLVISISRDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVT
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Sialic acid binding immunoglobulin-like lectin-E.
Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
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32.4%; Score 878; DB 2; Length 46
Best Local Similarity 39.0%; Pred. No. 1.4e-51;
Matches 204; Conservative 75; Mismatches 170; Indels
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STRAIN=C5/BL/6;
Zhang J.Q., Crocker P.R.;
"Characterization of mSiglecs-E and -F.";
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      OAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVKF 511
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                                                           293 HSSPPARLSWIQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Characterization of mSiglec-E, an inhibitory mouse Siglec expressed on cells of the innate immune system."; Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mousē).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                     Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.4%; Score 878; DB 2; Length 46
39.0%; Pred. No. 1.4e-51;
tive 75; Mismatches 170; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                             422 AAPSSTE--BEIHYATLSFHEMKPM-NLWGQQDTTTEYSEIKF
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02-WAR-2004 (TYEMBLrel. 27, Created)
02-WAR-2004 (TYEMBLrel. 27, Last sequence update)
02-WAR-2004 (TYEMBLrel. 27, Last annotation update)
Sialic acid binding 19-like lectin E.
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TISSUB-Mammary tumor metastatized to lung. MMTV-LTR/Wntl model.

Expression driven by an MMTV-LTR enhancer;

MEDINE-22388257; PubMed-1247932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J. Usdin T.B., Donaldo M.F., Casavant T.L., Scheetz T.B.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., MocBwan P.J., McKernan K.J., Malek J.A., Glubs R.A.,

Richards S., Worley K.C., Hale S., Garcinci P., Prange C.,

Richards S., Worley K.C., Hale S., Garcinci P., Prange C.,

Whiting M., Madan A., Young A.C., Shevichenko Y., Boulfard G.G.,

Mhiting M., Madan A., Young A.C., Shevichenko Y., Boulfard G.G.,

Minchaley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Mense S.J., Marra M.A.,

"Mense S.J., Ma
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342 QSSATL--SEMWAGTFVGSGVTALLFLSVCILLLAVRSYRKPARPAVVAPHP-----
                                                                                                                                    HISTORY SEPLESILE
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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STRAIN=Cacch II;
TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Whtl model.
Expression driven by an MMTV-LTR enhancer;
Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC023280; AA423280.1; -.
SEQUENCE 468 AA; 51987 MW; 26A0FF74D3CA4ACF CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                           468 AA.
                                                                                                                                    393 --DALKVSVSQNPLVESQADDS----
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121 AGLYFFRLERGK-TKYNYMMDKMTLVVTALTNTPQIILPETLEAGHPSNLTCSVPWDCGW 179
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                                                                                TAPPIFSWIGISVSFLSTNTIGS -- SVLIITPQPQDHGTNLTCQVTLPGTDVSTRMTIRL
                                                     CPPPSFSWTGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRL
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Search completed: November 5, 2004, 13:57:39 Job time : 116.542 secs

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Gaps
                                                                      sequence 14, sequence 14, sequence 14, sequence 84, sequence 84, sequence 84, sequence 34, sequence 2, sequence 2,
Patent No.
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32.8%; Score 888; DB 3; Length 43:
Best Local Similarity 47.8%; Pred. No. 1.5e-69;
Matches 195; Conservative 52; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 1
US-09-038-832-2
; Sequence 2, Application US/09038832
; Sequence 2, Application US/09038832
; Patent No. 6146845
; Patent No. 6146845
; THILE OF INVENTION:
; TITLE OF INVENTION: SIALOAGhesin Family Member-2
; TITLE OF INVENTION: SIALOAGhesin Family Member-2
; TITLE OF INVENTION: SIALOAGhesin Family Member-2
; TITLE OF INVENTION: SALOAGhesin Family Member-2
; TITLE OF INVENTION: SALOAGHES
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,832
FILING DATE: 11-MAR-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/041,886
FILING DATE: 02-APR-1997
ATTORNEY/AGENT INPORMATION:
NAME: PRESENCE/DOCKET NUMBER: 23,031
REFERENCE/DOCKET NUMBER: 23,031
REFERENCE/DOCKET NUMBER: 23,031
TELECOMMUNICATION INFORMATION:
                US-09-778-510-2
US-08-986-485-5
US-09-777-802-14
US-09-991-326-14
US-09-991-326-14
US-09-902-775A-84
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US-09-902-775A-84
US-09-906-700-84
US-10-140-002-348
US-09-906-716A-84
US-09-944-807-10
PCT-US93-603A-84
US-09-944-807-12
US-09-944-807-12
US-09-944-807-12
US-08-750-141A-2
US-09-944-807-12
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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amino acid
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; MOLECULE TYPE: protein
US-09-038-832-2
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  STRANDEDNESS:
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  Sequence 2, Appli
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Sequence 32, Appli
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Sequence 1, Appli
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Sequence 2, Appli
Sequence 38, Appli
Sequence 36, Appli
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Sequence 10, Appli
                                                                                                                                                                             November 5, 2004, 13:50:18; Search time 17.3484 Seconds (without alignments) 1957.231 Million cell updates/sec
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2706
1 Milpilissilggsqamdgr......RPEARMPKGTQADYAEVKFQ 512
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/cgr2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgr2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgr2_6/ptodata/1/iaa/8G_COMB.pep:*
/cgr2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
                            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-038-832-4

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US-08-896-537A-2

US-08-08-53-5

US-08-08-53-5

US-09-046-736-4

US-09-046-736-4

US-09-613-9990-7159

US-09-613-9990-7159

US-09-613-9990-7159

US-08-08-08-5

US-08-08-62-725-3

US-08-08-62-725-3

US-08-08-62-725-3

US-08-08-725-36

US-08-17-299-1

US-08-91-326-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -09-924-103-4
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                   using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match
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Perfect score:
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Result No.

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NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,
REFERENCE/DOCKET NUMBER:
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SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Diskett
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US-09-038-832-4
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| FVHGYWFRAGDRPYQDAPVAINNPDREVQAETYGRFQLLGDIWSNDCSLSIRDARKRDKG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  283 CAVNSNPPARLSWTRGSLTLCPSRSSNPGLLELPRVHVRDEGEFTCRAQNAQGSQHISLS 342
                                                                                    55 PAYGYWFKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDES 114
                                                                                                                                                                                                                                                                                                                                                                                239 VŘLDVSÝ------PPWNLTMTVFÖGDATASTALGNGSSLSVLEGGSLRLV 282
                             1 MLILILLIPLINGTKGMEGDRQYGDGYLLQVQELVTVQEGLCVHVPCSFSYPQDGWTDSD 60
  MLLPLLLSSLLGGSQAMDG-----RFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGST 54
                                                                                                                                                                                                                                                       170 FEECPPPSFSWIGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: KIKLY, KRISTINE
APPLICANT: BRICKSON-MILLER, CONNIE
TITLE OF INVENTION: Sialoadhesin Family Member-2
TITLE OF INVENTION: (SAF-2)
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: RAINER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastGEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,832
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APPLICATION NUMBER: 60/041,886
FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09038832
Datent No. 6146845
GENERAL INFORMATION:
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TELEPHONE: 610-407-0700
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IBM Compatible
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TOPOLOGY: linear
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COMPUTER READABLE FORM:
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COMPUTER: IB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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61 PVHGYWFRAGDRPYQDAPVATNNPDREVQAETQGRFQLLGDIWSNDCSLSIRDARKRDKG 120
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                                                                                                                                                                            1 MILITILIEPLIMGTKGMEGDRQYGDGYLLQVQELVTVQEGECVHVPCSFSYPQDGWTDSD
                                                                                                                               1 MLLPLLLSSLLGGSQAMDG-----RFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGST
                                                                    34; Gaps
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Query Match
32.8%; Score 888; DB 3; Length 43:
Best Local Similarity 47.8%; Pred. No. 1.5e-69;
Matches 195; Conservative 52; Mismatches 127; Indels
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Patent No. 6090582
GENERAL INFORMATION:
APPLICANT: KIKLY, KRISTINE
APPLICANT: ERICKSON-MILLER, CONNIE
TITLE OF INVENTION: Slaloadhesin Family Member-3
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/046,736
FLING DATE: 24-MAR-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 24-MAR-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/041,885
FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
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TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
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121 ERGRDVKYSYQQNKLNLEVTALIEKPDIHFLEPLESGRPTRLSCSLFGSCEAGPPLTFSW 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --GIGITALLFLCLALIIM 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               400 GGINSDLKVSCKAWNIYGSQSGSVLLLQGRSNLGTGVVPAALGGAGVMALLCICLCLIFF 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                387 KILPKRRIQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPL-PPGAPS 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       460 LIVKARRKÓA-AGRÞEKMDDED------PIMGTITSGSRKKPWPDSPGDQASPPGDAP 510
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                                                                                                                                                                                                                                                                          TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
                                                                                                                                                                                                                                                                                                    61 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
                                                                                                                                                                                     ERGSYVRYNFWNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW
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             LLPLLLSSLL-GGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
                                                       1 MIPLILLPLIMGGSLQEXPVYELQVQKSVTVQEGLCVLVPCSFSYPWRSWYSSPPLYVYW
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US-08-759-628-4
US-08-759-628 4
Sequence 4, Application US/08759628
Patent No. 6225446
GENERAL INFORMATION:
APPLICANT: ALtumann, Scott W.
APPLICANT: Rock, Fernando L.
APPLICANT: Rast, J. Fernando L.
APPLICANT: Kastelein, Robert A.
TITLE OF INVENTION: MUTATIONAL VARIANTS OF MAMMLIAN PROTEINS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
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STREET: 901 California Avenue
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ZIP: 94304-1104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Palining
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FILING DATE: 05-DEC-1996
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STATE: California
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                                                                                                                                                                                                                                      2 LIPILLISSILGGSQAMDGR----FWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTP
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                                                                                                                                                Score 831.5; DB 3; Length
Pred. No. 1.5e-64;
3; Mismatches 174; Indels
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29.6%; Score 800.5; DB 4;
Best Local Similarity 33.7%; Pred. No. 1e-61;
Matches 205; Conservative 71; Mismatches 172;
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Patent No. 659008
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Gentz, Reiner L.
APPLICANT: Gentz, Reiner L.
APPLICANT: Gentz, Reiner L.
APPLICANT: Rosen, Craig A.
TILE DE INVENTON: CD33-Like Protein
FILE REFERENCE: 1488.0480001
CURRENT APPLICATION NUMBER: 05/08/896,537A
PRIOR APPLICATION NUMBER: 60/022,481
PRIOR APPLICATION NUMBER: 60/022,481
PRIOR PILING DATE: 1996-07-19
PRIOR FILING DATE: 1996-07-19
SOFTWARE: Patentin version 3.1
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Best Local Similarity 37.9%; Pr
Matches 198; Conservative 78;
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467 amino acids
                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                              MOLECULE TYPE: protein US-09-046-736-2
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ORGANISM: Homo sapiens
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US-08-896-537A-2
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Patent No. 6225446

GENERAL INFORMATION:

APPLICANT: Rock, Fernando L.

APPLICANT: Rock, Fernando L.

APPLICANT: Kastelein, Robert A.

APPLICANT: Kastelein, Robert A.

APPLICANT: MATIONAL VARIANTS OF MAMMILIAN PROTEINS

TITLE OF INVENTION: MUTATIONAL VARIANTS OF MAMMILIAN PROTEINS

CORRESPONDENCE: ADDRESS:

ADDRESSEE: DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ***Query Match 28.4%; Score 769; DB 3; Length 440; SBest Local Similarity 36.5%; Pred. No. 4.3e-59; Matches 190; Conservative 73; Mismatches 163; Indels
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                                                                                                     NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0552Q
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 115-852-9196
TELEFAX: 415-496-1200
                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                         440 amino acids
                                                                                                                                                                                                                                       TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                               single
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                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: six
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MS-08-759-628-5
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281 LSWFQGSPAINATPISNTGILEIRRVRSAEEGGFTCRAQHPLGFLQIFLNLSVYSLPQLL 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53; Mismatches 132; Indels
                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.6%; Score 693.5; DB 3; 43.0%; Pred. No. 1.7e-52;
                                                                                                                                                                                                                                                                                                         PROGRAPHICATION DATA:
APPLICATION NUMBER: US 60/008,574
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTATION NUMBER: 34,090
REFERRUCE/DOCKET NUMBER: DX05520
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                          UMBER: US/08/759,628
05-DEC-1996
                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 421 amino acids
TYPE: amino acid
STRANDEDNESS: single
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APPLICANT: Gentz, Reiner L.
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         415-496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
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MOLECULE TYPE: protein
                                             ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                              FILING DATE: 05
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         341 GPSCS 345
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                      COUNTRY:
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MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                   61 FKAVTETTKGAPVATNHQSREVEMSTRGRPQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 LVISISRDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPARL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 SWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHYKKGLIS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 TAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINVVPTAG 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 ERGS-TKYSYKSPQLSVHVTDLTHRPKILIPGTLEPGHSKNLTCSVSWACEQGTPPIFSW 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------NPTTGIFPG-----DGS-----GKQET-----RAGLV- 258
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                                                                                                                                                                                                                                                                                                                                                                    1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
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                                                                                                                                                                                                                                                                       Query Match 25.6%; Score 693; DB 4; Length 364; Best Local Similarity 33.2%; Pred. No. 1.5e-52; Matches 170; Conservative 59; Mismatches 135; Indels 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09046736
Patent No. 6090582
GENERAL INFORMATION:
APPLICANT: KIKLY, KRISTINE
TITLE OF INVENTION: Sialoadhesin Family Member-3
TITLE OF INVENTION: Sialoadhesin Family Member-3
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: P.O. Box 380
CITY: Valley Forge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481 HYATLNFPGVRPRPEARMPKGTQADYAEVKFQ 512
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APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: CD33-Like Protein
FILE REFERENCE: 1489 048001,
CURRENT APPLICATION NUMBER: US/08/896,537A
CURRENT FILING DATE: 1997-07-18
PRIOR APPLICATION NUMBER: 60/022,481
PRIOR FILING DATE: 1996-07-19
PRIOR FILING DATE: 1996-07-19
SOFTWARE: Patentin version 3.1
SEQ.ID NO 3
                                                                                                                                                                                                                                                                                          Best Local Similarity 3.2.2. Matches 170; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                       US-08-896-537A-3
                                                                                                                                                                                    364
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US-09-046-736-4
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296 PPARLSWIQRGQVLSPSQPSDPGVLELPRVQVEHEGEFICHARHPLGSQHVSLSLSVHYK 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 YAPRDLVISISRDNTFDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSS 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----KGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHS 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294 -----AADVGDIGMK-------DANTIRGSASQGNLTESWADDNPRHH 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248 YIGKWRPVSGVLL----GAVGCAGATALVFLSFCVIFIVV---RSCRKKSARP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 AYGYWFKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 PPARLSWTWRSLTLYPSQPSNPLVLEL-QVHLGDEGEFTCRAQNSLGSQHVSLNLSLQQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 LLPLLLSSLLGGSQAMDGR-----FWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 YEERVERGSYVRYNEMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 21.2%; Score 573; DB 3; Length 374;
Best Local Similarity 29.8%; Pred. No. 5.4e-42;
Matches 156; Conservative 63; Mismatches 138; Indels 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              468 TQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK 510
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                  COMPUTER: IBM Compatible
CORRATING SYSTEM: DOS
SOFTWARE: FASESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/046,736
FILING DATE: 24.MAR.1998
CLASSIFICATION: 24.MAR.1998
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/041,885
FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 33,031
REGISTRATION NUMBER: 34.MAR.1997
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7159, Application US/09513999C Patent No. 6783961
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SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                              610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 610-407-0701
TELEFAX: 610-407-0701
TELEX:
Diskette
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SEQ ID NO 4599 LENGTH: 56 TYPE: PRI

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168 KPLSE-----IHSGNSVSLQCDFSSSHPK--EVQFFWEXNGRLLG----KESQLNF 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 TALTOKEDOYIPETLEPGOPVTVICVENWAFEECPPPSFSW--TGAALSSQGTKPTTSHF 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              373 ITALLFLCLALIIMKI----LPKR--RTQTET-------PRPRFSRHSTILDYIN 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 501;
                                                                                                                                                                                                     1 MILPELLSSILGGSQAMDGRFWIRVQESVWVPEGLCISVXLLFLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Chinnadurai, Govindaswamy
TILLE OF INVENTION: APOPTOPSIS-REGULATING PROTEINS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
GURENT APPLICATION DATA:
APPLICATION NUMBER: US/ns/^^
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALUKESSEE: SUCHRUE, MION, ZINN, MACPEAK & SEAS STREET: 2100 Pennsylvania Avenue, N.W. STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
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Best Local Similarity 20.0%; Pred. No. 4.3e-07;
Matches 107; Conservative 82; Mismatches 182;
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 31, Application US/08408095
Patent No. 5858678
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICAL....
FILING DATE: 21-MAR-199-CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mack, Susan J.
REGISTRATICN NUMBER: 30,951
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: (202)293-7060
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
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D.C.
USA
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GENERAL INFORMATION:
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
APPLICANT: Glordano, J.Y.
APPLICANT: Glordano, J.Y.
PITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
PILE REPERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR APPLICATION NUMBER: US 60/122,487
NUMBER OF SEQ ID NOS: 36681
SOPTWARE: PALENT.PM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 56;
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OTHER INFORMATION: score 11.3
OTHER INFORMATION: seq PILLISSLIGGSQA/MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4599, Application US/09513999C
Patent No. 6783961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Xaa=His or Gln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Xaa=Ala or Ser
US-09-513-999C-4599
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FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  191 KPTT 194
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NAME/KEY: UNSURE
LOCATION: 28
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NAME/KEY: UNSURE
LOCATION: 24
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GENERAL INFORMATION
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                                                                                                                                                                                                                                                     APPLICANT: Stern, David M.
APPLICANT: Schmidt, Ann Marie
APPLICANT: Schmidt, Ann Marie
APPLICANT: Schmidt, Ann Marie
APPLICANT: Schmidt, Ann Marie
TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND
TITLE OF INVENTION: USES THEREOF
FILE REPRENCE: 0575/62175
CURRENT APPLICATION NUMBER: US/09/638,649
CURRENT APPLICATION DATE: 2000-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
                                                       461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GQPVTV-ICVFNWAFEECPPPSFSW--TGAALSSQGTK------PTTSHFSVLS-F 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             322 LPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHY------KKGLISTAFSNGA 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----VGAILWRKR 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----APESQEDEEE--RAELN- 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 SVPNKVGTCVSEGSY---PAGTLSWHLDGKLLIPDGKETLVKEETRRHPETGLFTLRSEL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192 İVIPTOGGTİHPİFSCSFS-LGLPRRRPLNT----APIQL-----RVREPGPPEGIQLLV 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SQANRIVLENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLE 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 EPEGGI-------VAPGGTVTLTCAISAQPPPQVHWIKDGAPL-PLAPSP--VLL 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      368 FLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINVVPTAGPLAQKRN 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                428 OKATPNSPRTPLPPGAPSPESKKNOKKOYQLPSPPEPKSSTQAPESQESQEELHYATLNF 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 NCSLVIRDAQMQDESQYFFRV--ERGSYVRYNFMNDGFFLKVTALTQKPDVXIPET-LEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPRP-QDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVISISRDNTPDPPENLRVMV
                                                     102 SLGCYNPMMEDGISYTTLRFPEMNIPRTGDAESSEMORPPRTCDDTVTYSALHKRQVGDY
                                                                                         Q--LPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPRPRARMPKGTQADYAEVK 510
                                                                                                                          462 ENVIPOFPE-----DEGIHYSELIQFGVGERPQAQ----ENVDYVILK 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46; Mismatches 139; Indels 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.4%; Score 172.5; DB 4; Length 403; 23.3%; Pred. No. 8.7e-07;
                 415 VVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          347 LGGLGVVÁLL------
                                                                                                                                                                                                                  Sequence 5, Application US/09638649
Patent No. 6563015
GENERAL INFORMATION:
APPLICANT: Stern, David M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           488 PGVRPRPEARMPK 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local_Similarity
Matches 101; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 5
LENGTH: 403
                                                                                                                                                                                  RESULT 12
US-09-638-649-5
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                                                                                         457
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RESULT 13 US-08-602-725-32 'Sequence 32, Application US/08602725 'Patent No. 5965/10

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110 MQDESQYFFRVERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWA 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEECPPDSFSWTGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRT 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----GOSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHAR 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190 -RLOLSNGRITLILLSVTRNDTGPYECEIQNPVS-ANRSDPVTLNVTYGPDTPIISPSDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 -PELPKPS-----ISSNNSNPVEDKDAV-AFICEPETQDTTYLWWINNQSLPVSP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 LLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVP-----CSFSYPRQDWTGSTPAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 LLTASLL-----TFWNPPTTAQLTTESMPFNVAEGKEVLLLVHNLPQQ-----LF
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                                                                                                                                                            TITLE OF INVENTION: MONOCLONAL ANTIBODIES FOR USE IN
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
6.2%; Score 167; DB 2; Length 464;
Best Local Similarity 23.5%; Pred. No. 3.2e-06;
Matches 85; Conservative 52; Mismatches 122; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,725
FILING DATE: 02-FEB-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB94/01816
FILING DATE: 19-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9317423
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 ONDIGFYTLOV----IKSDLVNE----EATGOFHVY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY, MODELS.
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36663
REFERENCE/DOCKET NUMBER: 1090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4091
                                                    SNARY, DAVID
STEWART, LORNA MD
YOUNG, SUSAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 32: SEQUENCE CHARACTERISTICS: LENGTH: 464 amino acids
WALTER
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amino acid
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MOLECULE TYPE: protein
US-08-602-725-32
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                                                                                                                                          BATES
                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 22201
                                                                            APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Schmidt, Ann Marie
APPLICANT: Schmidt, Ann Marie
APPLICANT: Yan, Shi Du
TITLE OF INVENTION: TRANSCENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
TITLE OF INVENTION: GLYCATHEROF PERFORMENT APPLICANT APPLICANT APPLICANT APPLICANT APPLICATION NUMBER: US/09/638,649
CURRENT APPLICATION NUMBER: US/09/638,649
CURRENT FILING DATE: 2000-08-14
NUMBER OF SEQ 1D NOS: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 MQDESQYFFRVERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 FEECPPPSFSWTGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRT 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 -PELPKPS-----ISSNNSNPVEDKDAV-AFTCEPETQDTTYLWWINNQSLPVSP--- 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          190 -RLQLSNGNRTLTLLSVTRNDTGPYECEIQNPVS-ANRSDPVTLNVTYGPDTFTISPSDT 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283 ----GOSICIVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHAR 338
 248 YYRPGANLSLSCYAASNPPAQYSWLINGTFQQSTQE-----LFIPNITVNNSGSYTCHAN 302
                                                                                                                                                                                                                                                                                                                                                                                                                                            58 GY-WFKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKG-----NCSLVIRDAQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 GYSWYKG--ERVDGNSLIVGY-----VIGTQQATPGPAYSGRETIYPNASLLIQNVT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248 YYRPGANLSLSCYAASNPPAQYSWLINGTFQOSTQE----LFIPNITVNNSGSYTCHAN 302
                                                                                                                                                                                                                                                                                                                                                                      *Query Match 5.7%; Score 155; DB 6; Length 321; Sebst Local Similarity 24.3%; Pred. No. 2.2e-05; Matches 73; Conservative 43; Mismatches 105; Indels 80; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230 VRLRVAYAPRDL-VISISRDNTPDPPENLRVMVSQANRT--VLENLGNGTSLPVLE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 153.5; DB 4; Length 416; Pred. No. 4.2e-05;
                                                                                                                                                                                 APPLICANT: WAI-YEE, CHAN
TITLE OF INVENTION: PREGNANCY SPECIFIC PROTEINS APPLICATIONS
NUMBER OF SEQUENCES: 48
NUMBER OF SELICATION
APPLICATION NUMBER: US/07/390,409
FILING DATE: 07-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 QNDTGFYTLQV----IKSDLVNE-----EATGQFHVY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09638649
Patent No. 6563015
GENERAL INFORMATION:
APPLICANT: Stern, David M.
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, ORGANISM: BOS Taurus
US-09-638-649-1
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Best Local Similarity
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                                                        --AKGNCSLVIRDAQ 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---GLISTAFSNGAFLGIG 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303 PEDQGTYSCVATHPSHGPQESRAVSVTIIETGEBGTTAGSVEGPGLETLALTLGILGGLG 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  373 ITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNQKATP 432
                                                                                                                                                                                   110 MQDESQYFFRV--ERGSYVRYNFWNDGFFLKVTALTQKPDVYIPET-LEPGQPVTV-ICV 165
                                                                                                                                                                                                                              145 SEGGY----PAGTLNWLLDGKTLIPDGKGVSVKEETKRHPKTGLFTLHSELMVTPARGG-- 199
                                                                                                                                                                                                                                                                                                                                                                                                                                  211 IDLICHVDFS---RKGVSAQRIVRLRVAYAPRDLVISISRDNIPDPPENLRVMVSQANRI 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---ALHPTFSCSFTPGLPRRRAIHT----APIQLRVWSEHRGGEGP--NVDAVPLKEVQL 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                268 VLENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPG-VLELPRVQ 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -- RKGQERKVP 387
                                                                                                                32 KPLVLNCKGAP-KKPPQQLEWKLNT-GRTEAWKVLSPQGDPWDSVARVLPNGSLLLPAVG 89
57; Mismatches 170; Indels 125; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             433 NSPRTPLPPGAPSPESKKNOKKOYQLPSFPE-PKSSTQAP 471
                                                           62 KAVTETTKGAPVATNHQSREVEMSTRGRFQL-----TGDP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              327 VEHEGEFTCHARHPLGSOHVSLSLSVHYKK---
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   Conservative
   108;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 5, 2004, 13:50:17 ; Search time 14.2346 Seconds (without alignments) 3460.797 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-937-636-3 2706 1 MLIPLLLSSILGGSQAMDGR.....RPEARMPKGTQADYAEVKFQ 512

Scoring table:

283416 segs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	myeloid cell surfa	soform	in-	n cell	myelin-associated	myelin-associated	myelin-associated	sialoadhesin - mou	differentiation an	CD22 homolog/B lym	B-cell adhesion pr	ü	lycopro	probable advanced	perlecan precursor		biliary glycoprote	biliary glycoprote	rane car	pregnancy-specific	heparan sulfate pr	advanced glycosyla	nephrin - human	5	vascular cell adhe	hypothetical prote	н	ᅩ	ecif
SUMMARIES		A30521	152590	A61084	JH0593	BNRT3	BNRT3S	B33785	S50065	I49583	A46512	A35648	JH0371	A32164	T09062	A38096	JH0395	JH0396	JH0394	C30127	C27658	S18252	A42879	T37190	JC4122	JC2457	T20992	T43290	S68235	JN0067
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titin, cardiac mus	carcinoembryonic a	neural cell adhesi	vascular cell adhe	pregnancy-specific	poliovirus recepto	poliovirus recepto	pregnancy-specific	pregnancy-specific	biliary glycoprote	Lutheran blood gro	pregnancy-specific	advanced glycosyla	carcinoembryonic a	pregnancy-specific	pregnancy-specific
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144.5 5.3 26926	5.3		5.2	5.2	5.2	5.2		5.2	5.2	5.2	5.2	5.1	5.1		5.1

ALIGNMENTS

	RESULT 1 A305LT Myeloid cell surface antigen (C;Species: Homo sapiens (man) (;Date: 01-Dec-1989 #sequence, Ascression: A30521	antigen CD33 precursor - human ens (man) #sequence_revision 01-Dec-1989 #text_change 09-Ju1-2004	
	R.Simmons, D.; Seed, B. J. Immunol. 141, 2797-2800, 1988 A.Title: Isolation of a cDNA encoding A,Reference number: A30521; MUID:89009	CD33, a differentiation antigen of 814; PMID:3139766	myeloid progenit
	A;MOlecule type: mRNA A;Molecule type: mRNA A;Cross-references: UNIPROT:P2013:	A IM> UNIPROT: P20138	
	A; Gross-references:	GDB:119762; OMIM:159590	
	A; Map position: 134 C; Keywords: glycopr F; 1-17/Domain: sign	map postruon: 19413-11943-1 map postruon: 19413-11943-1 Keywords: glycoprotein; surface antigen; transmembrane protein 11-17/Domain: sorra-dillar #status predicted ASIG>	
	F;260-282/Domain: transmembrane #F;260-282/Domain: transmembrane #F;283-364/Domain: intracellular #F;100,113,160,209,230/Binding site	260-287/Domain: transmembrane #status predicted <tmm's 283-384/Domain: transmembrane #status predicted <tmm's 283-364/Domain: intracellular #status predicted <cyt> 100,113,160,209,230/Binding site: carbohydrate (Asn) (covalent) #status predicted</cyt></tmm's </tmm's 	ted
	Query Match Best Local Similarity Matches 168; Conserv	25.6%; Score 694; DB 2; Length 364; .larity 32.8%; Pred. No. 1e-39; .Conservative 59; Mismatches 137; Indels 148; Gaps 8;	
	Qy 1 MLLPL Db 1 MPLLL	MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW 60	
	Qy 61 FKAVT : Db 61 FREGA	FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120 	
	Qy 121 ERGSY Db 121 ERGS-	BRGSYVRYNFMNDGFFLKVTALTOKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW 180 : :	
 	Oy 181 TGAAL 	TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 240	
	241	DNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPARL $ \cdot $	-
	238		
	Db 248	SWICKGÇULSFSÇPEDIPGVLEHEGEFICHARHPLGSÇHVSLSLSUSVAYKAKELIS 360	

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human myelin-associated glycoprote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C. Superfamily: myelin-associated glycoprotein; immunoglobulin homology C. Keywords: brain; cell adhesion; glycoprotein; phosphoprotein; transmembrane protein; F.1-19/Domain: signal sequence #status predicted <SIG>F.1-19/Domain: signal sequence #status predicted <SIG>F.20-626/Product: myelin-associated glycoprotein #status predicted <MAT>F.35-102/Domain: immunoglobulin homology <IPM>F.35-102/Domain: immunoglobulin homology <IPM>F.35-102/Domain: immunoglobulin homology <IPM>F.35-102/Domain: cell attachment (R-G-D) motif F.514-536/Domain: transmembrane #status predicted <IPM>F.514-536/Domain: transmembrane #status predicted <IPM>F.599.223,246,315,406,450,454/Binding site: carbohydrate (Asn) (covalent) #status predicted respectively flanding site: carbohydrate (Asn) (covalent) #status predicted F.543,607/Binding site: phosphate (Ann) (covalent) #status predicted F.533/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Residues: 84-98,'X',100-110,210-222,'X',224;245,'X',247-253;309-318,'XXX',396-405, 38 (Comment: This protein is a neural cell adhesion molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 KGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRVERGSYVRY 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----SQANRIV-----LENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSW 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TORGOVISPSOPSDEGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHYKKGLI--- 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HCAAARDTVQCLCVVKSNPEPSVAFELPSRNVTVNESERBFVYSERSGLVLTSILTL--- 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 FWIMISASRGGHWGAWMPSSISAFEGTCVSIPCRPDFP--DELRPAVVHGVWYFNSPYPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NFMNDGFFLKVTALTOKPDVYIPETLEPGOPVTVICVFNWAFEECPP--PSFSWTG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RDLVISIS------PENLRVMV-----
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                                                                                                                                                                                                                                                                                                                                                     A, KOTOSE-references: GB: M29273; NID: g187292; PIDN: AAAS9545.1; PID: g307156
R; Burger, D.; Pidoux, L.; Steck, A.J.
Biochem: Biochem: Commun. 197, 457-464, 1993
A; Pitle: Identification of the glycosylated sequens of human myelin-assoc A; Reference number: PC2011; MUID: 94092116; PMID: 7505568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.3%; Score 304.5; DB 1; Length 626; 21.1%; Pred. No. 4.9e-13; ive 90; Mismatches 229; Indels 193;
                                                                                                                                                                                                         Reference number: A33263; MUID:89392063; PMID:2476987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----QKRNQKATPNSPRTPLPP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: GDB:120702; OMIM:159460
                                                                                                                                                                                                                                                                                     Molecule type: mRNA;Residues: 1-613,'T',615-626 <SAT>
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Best Local Similarity 21.18
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: GDB:MAG; GMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATILLE: Molecular cloning of two isoforms of the murine homolog of the myeloid CD33 and M.Reference number: 152590; MUID:94250900; PMID:8193354
AsAccession: 152590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.Status: not compared with conceptual translation
A.Status: not compared with conceptual translation
A.Status: 1-626 <SPA>
A.Status: 1-626 <SPA>
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A.Status: 1-626 <SPA>
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                                                                                                                                                                                                                                                                                                                                 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 LEKGVSLHEDSPVATSDPRQLVQKATQGRFQLLGDPQKHDCSLFIRDAQKNDTGMYFPRV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .21 ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 VREPPVRYSYKKSQLSLHVTSLSRTPDIIIPGTLEAGYPSNLTCSVPWACEQGTPPTFSW 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59
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C;Species: Homo sapiens (man)
C;Apecies: Homo sapiens (man)
C;Accession: A61084; A33263; PC2011
R;Spagnol, G.; Williams, M.; Srinivasan, J.; Goller, J.; Bauer, D.; Lebo, R.
Wheurosci, Res. 24, 137-142, 1989
A;Ritle: Molecular cloning of human myelin-associated glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ୍ୟୁସ୍ଥିତ୍ୟତ୍ତ Mus sp. (mouse)
ରମ୍ମହ୍ୟତ: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 TAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINVVPTAG
                                                                                                                                                                                                                                                                                                                                 ----HGAIGGAGVTALLALCLCLIFFIVKTHRRKAARTAVGRNDTH-----PTTG
                                                                                                                                                                                                                                                                                                                                                                                                          421 PLACKRNOKATPNSPRTPLPPGAPSPESKKNOKKOYQLPSFPEPKSSTQAPESQESEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -- TETSSCSGAAPTVEMDEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Across-references: GB:S71345; NID:g551352; PIDN:AAB30842.1; PID:g551353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --NVTRKSGQMRELVLVAVGEATVKLLILG--LCLV 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.5%; Score 528; DB 2; Length 40
42.2%; Pred. No. 2.1e-28;
tive 34; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .; Beverley, P.C.; Young, B.D.; Watt, S.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apstatus: preliminary; translated from GB/EMBL/DDBJ Apmolecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   339 HYASLNFHGMNP----SKDTSTEYSEVRTQ 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYATLNFPGVRPRPEARMPKGTQADYAEVKFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 42.2
Matches 122, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  305 SASPKHOKKSKLHGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ChAccession: IS2590
Refebilian, E.Z.; Beverley
Blood 83, 3188-3198, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARRESIGNES: 1-403 <RES>
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462 PEPKSSTQAPESQESQBELHYATLNFPGVRPRPEARMPKGTQADYAEVK 510 ::: : : : :	QY 407STILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQ 452 bb 514 VGPVGAVVAFAIVIAVVCYLSQSRRKKGAGSPEVTPVQPMAGPGGDPDLDLRPQQVRWLR 573
4 LINS	453KKOYOLPSFPEFKSSTQAPESOESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK 51
593 worden cell myelin protein precursor - Japanese quail pecies: Coturnix coturnix japonica (Japanese quail) ate: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004	DD 574 GAMERWALGVKEGSGAPQEVIPISHIRGFLEDPPEYABIR 018 RESULT 5
; Marshak, D.R.; Roder, J.; Le	BNR13 myelin-associated glycoprotein precursor, long splice form - rat N.Alternate names: 18236; brain neuron cytoplasmic protein 3; MAG
aracterization of the schwann cell myelin protein, SMP: structural HOS93; MUID:92153423; PMID:1739462	C;Species: Rattus norvegicus (Norway rat) C;Date: 19-reb-1894 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004 C:Accession: A29028: A94175: A27185: A90836; I56564; I52882; A03138; A26362
1; PID:9245730	Rilai, C.; Brow, M.A.; Nave, K.A.; Noronha, A.B.; Quarles, R.H.; Bloom, F.E.; Milner, R.; Proc. Natl. Acad. Sci. U.S.A. 84, 4337-4341, 1987 Ajritle: Two forms of 18256/myelin-associated glycoprotein, a cell adhesion molecule for a bear manhar. Algorith with 1923-2001. DWIND-2438699
	A. Accession: A29028 A. Accession: A29028 A. Fordenie Lype: MRNA
Residuae 172: plocan Residuaes: 18-31;119-132;135-157;563-569,'X',571 <duli> Comment: This protein is expressed on all external membranes of Schwann cells. Superfamily: myelin-associated divcorpretein: immunodiobulin homology</duli>	A, TCSILGGES - LAIL - LOS - LAIL - LOS - LAIL - LOS -
•	A,Title: Molecular cloning and primary structure of myelin-associated glycoprotein. A,Reference number: A94175; MUID:87092455; PMID:2432614
	A,Molecule type: mRNA A,Molecule type: mRNA A,Residues: 1-626 <arq></arq>
predicted	A, Cross-references: GB:M14871; NID:g205267; PIDN:AAA41556.1; PID:g205268 R;Salzer, J.L.; Holmes, W.F.; Colman, D.R.
Query March 11.2%; Score 302.5; DB 2; Length 620; Best Local Similarity 22.4%; Pred. No. 6.6e-13; Matches 148; Conservative 89; Mismatches 224; Indels 199; Gaps 29;	J. Cell BLOL. 104, 357-365, 1987 A.Title: The amino acid sequences of the myelin-associated glycoproteins: homology to the A.Reference number: A27185; MUID:87166195; PMID:2435742
SILLGGSQAMDGREWIRVQESVAVPEGLCISVPCSFSYPRQDWTGSTPAYGYWFK 62	A.Accession: A27185 A.Molecule type: mRNA A.Molecule type: mRNA
::::::::::::::::::::::::::::::::::::::	Afcrose-references: GB:X05301; NID:g56611, PIDN:CAA28920.1; PID:g56612 R/Sutcliffe, J.G.; Milner, R.J.; Shinnick, T.M.; Bloom, F.E.
63 AVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDE- 113	Cell 33, 671-682, 1983 A,Title: Identifying the protein products of brain-specific genes with antibodies to chen A,Reference number: A90836, MUID:83259254, PMID:6347394
172	A.Accession: A90836 A.Molecule type: mRNA A.besiduse: 'K2' 311.656 cffm.
111 AGKYYFRGDLGGYNQYSF-SEHAELDVWAAPHLEVPHELVAGSEAEILCRVPDN 163	Ajkusiuutes: NS /JII-620 (2017) Ajkuses-references: GB:V01544; GB:J00756; NID:g56879; PIDN:CAA24786.1; PID:g818027 Likynesimental cource: Clone 178236
CPPPSFSWTGAALSSQGTKPTTSHF8VLSFTPRPQDHDTDLTCHVDFSRK 222	A.Note: the authors translated the codon CAG for residue 350 as Asn R;Bloom, F.E.; Battenberg, E.L.F.; Milner, R.J.; Sutcliffe, J.G.
CPPLKPLLTWTGTEELLDPIGKERIEDDLGSKSLLGSLRFRPRKEDLGRRVGCGVTFINS 223	J. Neurosci. 5, 1781-1802, 1985 Aprile: Immunocytochemical mapping of 18236, a brain-specific neuronal polypeptide deduc
GLWGPTEVVEGSDVELGCEAEGRPAPLISWFRGSEVLREEP 283	Affacted number: 19994; Noth: 952097; Filt 195047; Affacted number: 196564 Affacts: preliminary; translated from GB/EMBL/DDBJ
254 PENLRVMVSQANRTVLEN	A;Molecule type: mkNA A;Residues: KSY,311-626 <res> A;Cross-references: GB:M36702; NID:q203181; PIDN:AAA40831.1; PID:q203182</res>
GRNIRLLLSNVGPDDGGSFSCVAENRHGRHNRSLQLRVAYAPRAPVING-SLWVVSGDPV 342	R;Sutcliffe, J.G.; Milner, R.J.; Bloom, F.E. Cold Spring Harb. Symp. Quant. Biol. 48, 477-484, 1983
287 CLVCVTHSSPPARLSWTORGOVLSPSQPSDPGYLELPRVQVEHEGEFTCHARHPLGSQHV 346 287 CLVCVTHSSPPARLTTTT 1 1 1 1 1 1 1 1 1	Ajittle: Celtular localization and function of the proteins encoded by Diali-Specific mar AjReference number: 152892; MUID:84206577; PMID:6586369 AjAccession: 152892
SLSLSVHYKKGLI 363	A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA
::	A, Residues: 'XS',311-626 <re2> A, Forsa-references: GB MIL121; NID:g206780; PIDN:AAA42082.1; PID:g206781 C. Commont. The commond contains fits pressimally extracellular domains that are distantly</re2>
SNGAFLGIGIT ALLFLCLALIIMKILPKRRTOTETPRPRFSRH 406	C.Comment: The long form predominates in early postnatal life, alternative splicing prodict. C.Comment: The papers cited variously predict the mature protein to begin at residue 17,
463 PPGSDGSITGI-LTLRGPLEPRLLVLCAARNRHGTTARQLRFHHPGGLVWAK 513	C;Genetics:

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90 % qq

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Molecule type: mRNA
Residues: 565-582 <TRO>
                                                                   A;Molecule type: mRNA
A;Residues: 1-582 <LAI>
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                                                           ### 1975 | Product: myelin-associated glycoprotein, long splice form #status predicted <a href="### 1975" | Product: myelin-associated glycoprotein, long splice form #status predicted <a href="## 1975" | Product: myelin-associated glycoprotein, long splice form #status predicted <a href="## 1975" | Product: myelin-associated glycoprotein, long splice form #status predicted <a href="## 1975" | Product: mmunoglobulin homology <a href="## 1975" | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production | Production |
                                   glycoprotein; trans
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myelin-associated glycoprotein; immunoglobulin homology ternative splicing; brain; cell adhesion; duplication; g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.9%; Score 295.5; DB 1; Length 626; 22.2%; Pred. No. 2e-12; ive 85; Mismatches 239; Indels 173.
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Natternate names: 18236; brain neuron cytoplasmic protein 3; MAG
CESPECIES: Rattus norvegicus (Norway rat)
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Superfamily: myelin-associated care words: alternative splicing;
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cf02fce: 30-Jun-1990 #sequence revision 30-Jun-1990 #text_change 16-Jun-2000 Cfaccession: B29028; B27185; A60055 "Briai, C.; Brow, M.A.; Nave, K.A.; Noronha, A.B.; Quarles, R.H.; Bloom, F.E.; Milner, R.

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Proc. Natl. Acad. Sci. U.S.A. 84, 4337-4341, 1987
A;Title: Two forms of 1B236/myelin-associated glycoprotein, a cell adhesion molecule fe
A;Reference number: A29028; MUID:87232001; PMID:2438699
A;Accession: B29028
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); Keywords: alternative splicing; brain; cell adhesion; duplication; glycoprotein; itslyDomain: signal sequence #status predicted <SIG>
); 1-9/Domain: signal sequence #status predicted <SIG>
); 20-582/Product: myelin-associated glycoprotein; short splice form #status predicted |
); 155-102/Domain: immunoglobulin homology <IRMI>
); 118-120/Region: cell attachment (R-G-D) motif |
); 254-219/Domain: immunoglobulin homology <IRMI>
); 340-394/Domain: immunoglobulin homology <IRMI>
); 254-307/Domain: immunoglobulin homology
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;Comment: The sequence contains five presumably extracellular domains that are discar;
;Comment: The short form is found in the adult; the long form predominates in eachy
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R;Salzer, J.L.; Holmes, W.P.; Colman, D.R.
J; Gell Biol. 104, 957-965, 1987
A;Title: The amino acid sequences of the myelin-associated glycoproteins: homology.
A;Reference number: A27185; MUID:87166195; PMID:2435742
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A,Residues: 149-582 <AL>
A,Residues: 149-582 <AL>
A,Residues: 149-582 <AL>
A,Cross-references: GB:X06554; NID:956614; PIDN:CAA29797.1; PID:91334302

B,Tropak, M.B.; Johnson, P.W.; Dunn, R.J.; Roder, J.C.

B,Tropak, M.B. Brain Res. 4, 143-155, 1988

A;Title: Differential splicing of MAG transcripts during CNS and PNS development.
A,Reference number: A60055
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                                                                                                   129 NEWNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPP--PSFSWTGAALS 186
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10.7%; Score 289.5; DB 1;
Best Local Similarity 23.2%; Pred. No. 4.6e-12;
Matches 110; Conservative 64; Mismatches 185;
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OY 363 FSNGAFLGIGITALLFLCLALIIMKLLPKRRIQTETPRPRFSRHSTI 409 DD 414IILLESHCAAARDIVQCLCVVKSNPEPSVAFELPSRNVTV 453	Db 357 LTIFKEKQILATVIYESQLQLELPAVTPEDDGEYWCVAENQYGQRATAFNLSVEFAP 413 Qy 360 STAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTI 409 And Andrew Companies of the control of the co
RESULT 7 B33765 myeline associated glycoprotein - mouse C,Species: Mus musculus (house mouse) C,Species: Mus rusculus (house mouse) C,Species: Musri990 #sequence revision 23-Mar-1990 #text_change 23-Jul-1999 C;Date: 22-Mar-1990 #sequence revision 23-Mar-1990 #text_change 23-Jul-1999 C;Accession: B33785, A33785, So5687; SO2374 R;Fujita: No.; Sato, S.; Kurihara, T.; Kuwano, R.; Sakimura, K.; Inuzuka, T.; Takahashi, Biophys. Res. Commun. 165, 1162-1169, 1989 A;Title: CDNA dloning of mouse myelin-associated glycoprotein: a novel alternative splic A;Accession: B33785 A;Accession: B33785 A;Accession: B33785 A;Accession: A33785 A;Accession: A33785 A;Accession: A33785 A;Status: preliminary	SULT 8 Joadhesin - mouse Species: Mus musculus (house mouse) Species: Mus musculus (house mouse) Species: Mus musculus (house mouse) Stocker, PR. MucKlow, S.; Bouckson, V.; McWilliam, A.; Willis, A.C.; Stocker, PR.; MucKlow, S.; Bouckson, V.; McWilliam, A.; Willis, A.C.; Stocker, PR.; MucKlow, S.; Bouckson, V.; McWilliam, A.; Willis, A.C.; Stocker, PR.; MucKlow, S.; Bouckson, V.; McWilliam, A.; Willis, A.C.; Stocker, PR.; MucKlow, S.; Bouckson, V.; McWilliam, A.; Willis, A.C.; Stocker, PR.; Mulb.; Souckson, Mulb.; Souckson, PRID: 7925291 Stocker, PR.; Mulb.; Sulp.; Mulb.; Souckson, PRID: 7925291 Stocker, PR.; Mulb.; Sulp.; Mulb.; Sulp.;
A; Molecule type: mRNA A; Residues: 1582 < FU3> A; Cross-references: GB:M31811; NID:g199016; PIDN:AAA39487.1; PID:g199017 R; FUjita, N.; Sato, S.; Kurihara, T.; Inuzuka, T.; Takahashi, Y.; Miyatake, T. R: FBS Lett. 232, 323-327, 1988 A; Title: Developmenteally regulated alternative splicing of brain myelin-associated glyco	Query Match Best Local Similarity 25.7%; Pred. No. 1.8e-08; Matches 107; Conservative 52; Mismatches 179; Indels 78; Gaps 14; Qy 5 LLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYWFKAV 64
A;Nolecule type: mRNA A;Nolecule type: mRNA A;Residues: 310-374;566-573,584-588 <fu2> A;Cross references: EMBL:X07849 A;Accession: S02374 A;Nolecule type: mRNA A;Residues: 310-374;566-582 <fu4> A;Cross references: EMBL:X07849</fu4></fu2>	65 TETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRVERGS
Cylentica: 7 CySuperfamily: myelin-associated glycoprotein; immunoglobulin homology CySuperfamily: myelin-associated glycoprotein; immunoglobulin homology CyKeywords: alternative splicing; glycoprotein; transmembrane protein F;152-219/Domain: immunoglobulin homology <imm2></imm2>	183AALSSQGTKPTTS-HFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYA 183AALSSQGTKPTTS-HFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYA
Query Match 10.7%; Score 288.5; DB 2; Length 637; Best Local Similarity 23.1%; Pred. No. 6e-12; Matches 110; Conservative 62; Mismatches 184; Indels 121; Gaps 14;	QY 238 PRDLVISISRDNTPDPPENLRVMVSQANRTVLENLG273
QY 21 FWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYWFKAVTETT 68	Qy 274
Qy 69 KGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDBSQYFFRVERGSSYNRY 128	QY 300 LSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVS-LSLSVHY 354
OY 129 NEWNDGFELKVTALTQKEDVYIETLEPGQPVTVICVENWAFEECPPPSFSWTGAALS 186 128 TFSEHSVLDIVNTPNIVVPPEVVAGTEVEVSCAWPDNCPELRPELSWLGHEGL 180 QY 187 SQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAP 238	RESULT 9 149583 differentiation antigen - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Accesion: 1096 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
239 RDLVISISRDNTPDP	R;Law, C. J. Immunol. 151, 175-187, 1993 A;Title: Organization of the murine Cd22 locus. Mapping to chromosome 7 and characterizat A;Reference number: 149563; MUID:93315834; PMID:8100843
OY 254PENLRYMYSQANRTVLENLGNGTSLPVLEGGSLCLVCVTHSSPPAR 299 Db 301 GVYACLAENAYGQDNRTVELSVMYAPWKPTVVAV-EGETVSILCSTQSNPDPI 356 OY 300 LSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHYKKGLI 359	A;Accession: 149583 A;Attus: preliminary; translated from GB/EMBL/DDBJ A;Attus: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mENA A;Residues: 1-862 <res> A;Cross_references: UNIPROT:P35329; GB:L16928; NID:g348965; PIDN:AAA02562.1; PID:g348966 C;Genetics: A;Genetics: A</res>

213 NVYT 239 272 NSVT 270E 270E 331 QASN 336 GQVI 306 GQVI		Ristamenkovic, I.; Seed, B. Nature 345, 74-77, 1990 A.Title: The B-cell antigen CD22 mediates monocyte and erythrocyte adhesion. A.Reference number: A35648; MUID:90231465; PMID:1691828 A.Accession: A35648 A.Molecule type: mRNA A.Residues: 1-647 <sta> A;Cross-references: GB:X52785; NID:g29778; PIDN:CAA36988.1; PID:g29779 C;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Gross-references: GB:L27545; OMIM:107266</sta>	A,Map position: 19q13.1-19q13.1 C,Keywords: alternative splicing, B-cell; cell adhesion; dimer; glycoprotein; transment C,Keywords: alternative splicing, B-cell; cell adhesion; dimer; glycoprotein; transment F,1-19/Domain: signal sequence #status predicted <bigs #status="" <ext="" domain:="" extracellular="" f,20-510="" predicted=""> F,512-484/Domain: immunoglobulin homology <imm> F,512-644/Domain: immunoglobulin homology <imm> F,5130-647/Domain: intracellular #status predicted <tmm> F,530-647/Domain: intracellular #status predicted <cyt> F,67,101,112,135,164,231,268,302,397,457/Binding site: carbohydrate (Asn) (covalent) and Cuery Match Query Match Best Local Similarity 19.0%; Pred. No. 2.2e-06; Matches 130; Conservative 87; Mismatches 212; Indels 257; Gaps 27;</cyt></tmm></imm></imm></bigs>	OY 1 MILPILISSILGGSQAMDGRFWI-RVQESVMVPEGLCISVPCSFSYPRQ 48	Qy 109 QMQDESQYFRYDERGSYVRYDFMNDGFFLKVTALTQKPDVYIPETLEPGQFVTVICVEN- 167	Qy 210 D
SS SS	127 AGTERWMEDIHLINVSEKPFÖPTIGHES SVITTGGLMFSCFEVDILLQWFL 182 171 EECPPSFSWTGAALSSQTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQR 228 183 EDSKITSVTPSVTSITSSVTNSTRNVYTESKLJFOPKWTDHGKSVKCQVQHSSE-VLSER 241 229 TVRLRVAYAP	OY 259 WWVSQANRTUL	RESULT 10 "A46512 "CD22 homolog/B lymphocyte-restricted adhesion molecule - mouse "CD22 homolog/B lymphocyte-restricted adhesion molecule - mouse "CD22 homolog/B lymphocyte-restricted adhesion nelecule - mouse "C) Species: Ms mucculus (house mouse) "C, Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1995 ©; Accession: A46512 R; Torres, R.M; Law, C.L.; Santos-Argumedo, L.; Kirkham, P.A.; Grabstein, K.; Parkhouse, J. Immunol. 149, 2641-2649, 1992 A; Title: Identification and characterization of the murine homologue of CD22, a B lymphoty. R; Reference number: A46512; MUID:93017867; PMID:1401903	As Accession: Adsize As Accession: Adsize As Status: preliminary; not compared with conceptual translation As Molecule type: nucleic acid As Residues: 1-868 < TOR> As Experimental source: B cell lymphoma 38Cl3 As Note: sequence extracted from NCBI backbone (NCBIP:116156) As Motery Match Best Local Similarity 21.7%; Pred. No. 3.6e-07:	EGL EGA EGA TRG	LKTHPIRANDSGNLGLR ICVEN TCGLNFSCFGYDILLER OTDLTCHVDFSRKGVSA :

oy Db	242VISISRDNTPDPPBNLRVMVSQANRTVLENL 272	& A	49 DWTGSTPAYGYWFKAVTETTKGAPVATNHQSREVEMSTRGRPQLTGDPAKGNCSLVIRDA 108 5:
Oy Db	273 GNGTSLPVLEGGSLCLVCVTHSSPPARLSWTQRQVLSP 311 	SP GS	109 QMQDESQYFFRVERGSYVRYNFWNDGFFLKYTALTQKPDVYIPETLEPGQPVTVICVFN- 167 10 H.NDSGQLGLRMESKTEKWMERIHLNVSERPFPPHIQLPPEIQESQEVTLTCLLNF 165
Qy Db	312 SQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLS-LSVHYKKGLISTAFSNGAFLG 370	& g	168WAFBECPPPSFSWTGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHV 217
çy Dp	371 IGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINVVPTAGPLAQ 424 :	\$ A	218 -DFSRKGVSAQRTVRLRVAYAPRDLVISISRDNTPDPPE 255 222 QDADGKFLSNDTVQLNVKHTPKLEIKVTPSDAIVREGDSVTMTCEVSSSNPEYTTV 277
O Dp	425 KRNOKATPNSPRTPLPPGAPSPESKKNOKKOYOLPSFPEPKSSTQAPESQESGEELHYAT 484	ð 93	256
Q Q	485 INFPGVRPRPEARMPKGTQADYAEVK 510	75 G	278LPVLEGGSLCLVCVTHSSP-PARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEF 333 : : : : : :
RESULT 12 JH0371 B-cell adhes	ion protein Cl	Oy QD	334 TCHARHPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALL 377
N, Alterna C, Species C, Date: 3 C, Accessic R, Wilson, J. Exp. M	NyAlternate names: B-cell membrane protein CD22 C.Species: Howo sapiens (man) C.Spacies: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 09-Jul-2004 C.Accession: JH0371; 156171 R.Wilson, G.L.; Fox, C.H.; Fauci, A.S.; Kehrl, J.H.	RESULT A32164 biliar N,Alte N,Cont	13 y glycoprotein 1 precursor, splice form a - human y glycoprotein 1 precursor, splice form a - human ains: biliary glycoprotein 1, splice form b; biliary glycoprotein 1, splice form x
A;Title: A;Referen A;Accessi: A;Molecul: A;Residues	cDNA cloning of the B cell membrane protein CD22: a mediator of B-B cell interaction of moder: JH0371; MUID:91086838; PMID:1985119 i. type: mRNA is: 1-847 <will></will>	C;Spec C;Date C;Acce R;Hino Proc.	C;Species: Homo sapiens (man) C;Date: 20-Apr-2000 #sequence revision 20-Apr-2000 #text_change 09-Jul-2004 C;Accesion A32164; A30127; A48078; S45664; S65939; A30847; G44476 E;Hinoda, Y.; Neumaier, M.; Hefta, S.A.; Drzeniek, Z.; Wagener, C.; Shively, L.; Hefta, I Proc. Natl. Acad. Sci. U.S.A. 86, 1668, 1989
A,Cross-r A,Experim A,Note: ti R,Wilson,	eferences: UNIPROT.060926, GB:X59350; NID:g36090; PIDN:CAA42006.1; PID:g36091 nental source: B lymphocyte authors translated the codon AAT for residue 358 as Met G.L.; Najfeld, V.; Kozlow, E.; Menniger, J.; Ward, D.; Kehrl, J.H.	A;Refe A;Cont A;Acce A;Mole	A,Reference number: A32164 A,Contents: erratum A,A,Coession: A32164 A,Molecule type: mRNA
J. Immuno A;Title: A;Referen	ol. 150, 5013-5024, 1993 Genomic structure and chromosomal mapping of the human CD22 gene.	A, Resi A, Cros R, Hino	A;Residues: 1-526 <hin> A;Cross-references: UNIPROT:P13688; GB:J03858; NID:g179439; PIDN:AAA51826.1; PID:g179440 R;Hinoda, Y.; Neumaier, M.; Hefta, S.A.; Drzeniek, Z.; Wagener, C.; Shively, L.; Hefta, I Droc, Narl Anad Sci II S A R5, 6956-6963: 1988</hin>
A; Accessi A; Status: A; Molecul	on: 1561/1 translated from GB/EMBL/DDBJ e type: DNA e type: DNA	A;Titl A;Refe	A.Title: Modernar cloning of a cDNA coding biliary glycoprotein I: Primary structure of A.Title: Modernar cloning of a cDNA coding biliary glycoprotein I: Primary structure of A.Refront number: A94206; MUID:88320555; PMID:2457922
A; Kesidue A; Cross-r C; Genetic		A; Note R; Barr	ents: annocation. : the sequence shown in this reference has been completely corrected in reference ? :: the sequence shown in this reference has been completely corrected in reference ? : the sequence shown in this reference has been completely corrected in reference ? : the sequence shown in this reference has been completely corrected in reference ? : the sequence shown in this reference has been completely corrected in reference ? : the sequence shown in this reference ? : the sequence shown in this reference has been completely corrected in reference ? : the sequence shown in this reference has been completely corrected in reference ? : the sequence shown in this reference ? : the sequence shown in this reference ? : the sequence shown in this reference ? : the sequence shown in this reference ? : the sequence shown in this reference ? : the sequence shown in this reference . : the sequence . : t
A;Gene: G A;Cross-r A;Map pos A;Introns		A; Titl A; Refe A; Acce	e: Carcinoembryonic antigens: alternative splicing accounts for the multiple mRNAs rence number: A92752; MUID:89139550; PMID:2537311 ssion: A30127
C; Keyword F; 1-19/Do F; 20-847/ F; 346-398 F; 609-661	phoprd	A, Mole A, Resi A, Cros A, Expe A, Acce	A,Molecule type: mRNA A,Residues: 1-526 <bar1> A,Cross-references: EMBL:X16354; NID:g37197; PIDN:CAA34404.1; PID:g37198; EMBL:X14784 A,Experimental source: splice form a A,Accession: B30127</bar1>
F;688-706 F;67,101, F;764,789	(coval	A;Mole A;Resi A;Cros	icule type: mRNA dues: 1-319, °D',417-526 <bar2> is-references: EMBL:X14831; NID:g37199; PIDN:CAA32940.1; PID:g37200; EMBL:X14784 rimental source: sollice form b</bar2>
Query Match Best Local Matches 9	7.5%; Score 202.5; DB 2; Length 847; Similarity 21.0%; Pred. No. 5.7e-06; 8; Conservative 69; Mismatches 182; Indels 117; Gaps 19;	R;Barr Mol. C A;Tit] A;Refe	<pre>lett, T.R.; Drake, L.; Pickle II, W. lell. Biol. 13, 1273-1282, 1993 lell. Biol. 13, 1273-1282, 1993 le: Human biliary glycoprotein gene: characterization of a family of novel alternati rence number: A48078, WUID:93140765; PMID:8423792</pre>
Ą Q Q	1 MLLPLLLSSLLGGSQAMDGRFWI-RVQESVMVPEGLCISVPCSFSYPRQ 48	A; Acce A; Mole A; Resi A; Cros	A,Accession: A48078 A,Moleonle Cype: mRNA A,Residues: 124-141,'H',417-526 <bar3> A,Cross-references: GB:M76742; NID:g179480; PIDN:AAA57142.1; PID:g179481</bar3>

3.nov04.rpr	Db 248 YYRPGANLSISCYAASNPPAQYSWLINGTFQOSTQELFIPNITVNNSGSYTCHAN 302 Qy 339 HPL-GSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCIA 382 : :	s, C.; Lasky, S.; Loretz llity locus class III re 2564945; PID:g2564950 ; 320/1; 329/1; 371/2 tor; immunoglobulin homo	Query Match 6.8%; Score 184; DB 2; Length 402; Best Local Similarity 23.4%; Pred. No. 4.1e-05; 100 NCSLVIRDAQMODESQYFRVERGSYURYNEWNDGFELKUTALTQKPDVYIPET-LEP 156 Qy 100 NCSLVIRDAQMODESQYFRVERGSYURYNEWNDGFELKVTALTQKPDVYIPET-LEP 156 Db 80 NGSLLLATGIUDEGTERCRATURRGKEWSUNYRPTTSHFSPLIA 134 QY 157 GQPVTV-ICVFWMAFECPPPSFSWTGAALSSQGTKPTTSHFSFLIA 134 Db 135 SVDWKVGTCVSEGSYPAGTLSWHILDGKLLIPDGKETLVKEETRRHPETGLFTLRSEL 191 QY 203 TPRPQDHDTDLTCHVDFSRKGVSAQFTVRLRVAXARRDLVISISRDNTPDPPENLRVWVS 262 Db 192 TVIPTQGGTHPTFSCSFS-LGLPRRRPENTTAPTQLRVREPGPPBGIGLIVE 241 QY 263 QANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTGRGQVLSPSOPSDFGVLEL 325 Db 242 PEGGI
Tue Nov 9 08:30:01 2004 us-09-937-636-3	Note: sequence extracted from NCBI backbone (NCBIN:123602, NCBIP:123606) Note: sequence extracted from NCBI backbone (NCBIN:123602, NCBIP:123606) Note: neither the complete nucleic acid sequence nor the complete translation are show a sequence. Balance, W.; Nedellec, P.; Turbide, C.; Stanners, C.P.; Barnett, T.R.; Beauchemin, N. Aritie: Transcriptional control of the human biliary glycoprotein gene, a CEA gene family setting type: DNA Nocession: 845644; MUID:9433343; PMID:805523 Nocession: 845646 Nocession: 845647; MUID:9433343; PMID:805923 Nocession: 85939; MUID:953447; PIDN:CAA47694.1; PID:8606777 Nocession: 86939; MUID:95354678; PMID:7628460 Anticle: Characterization and transcriptional activity of the mouse biliary glycoprotein procession: 86939; MUID:95354678; PMID:7628460 Anticle: Characterization and transcriptional activity of the mouse biliary glycoprotein procession: 86939; MUID:95354678; PMID:7628460 Anticle: Characterization and transcriptional activity of the mouse biliary glycoprotein procession: 86939; MUID:95354678; PMID:7628460 Anticle: Characterization and transcriptional activity of the mouse biliary glycoprotein procession: 86939; MUID:95354678; PMID:7628460 Anticle: Characterization not shown Anticle: Characterization and transcriptional activity of the mouse biliary glycoprotein procession: 86939; MUID:9529447; PIDN:CAA47694.1; PID:g606777 Notes: The sequence was submitted to the EMBL Data Library, July 1992 Note: Only a part of the coding sequence is given Anticle: Characterization of three new genes and estimation of the size of the carcinoembre sequence number: A44476; MUID:93052339; PMID:1427854 Note: Only a part of the capted sequence and estimation of the size of the carcinoembre sequence number: A44476; MUID:93052339; PMID:1427854	## Gene: GDB:BGP A Gross-references: GDB:127992; OMIM:109770 A Gross-references: GDB:127992; OMIM:109770 A Gross-references: GDB:127992; OMIM:109770 A Gross-references: GDB:12-19913.2 A Gross-references: alternative splicing: glycoprotein; surface antigen; transmembrane protein C Growords: alternative splicing: glycoprotein; surface antigen; transmembrane protein F):138/Domain: carcinoembryonic antigen predicted <sig> F):134/Domain: signal sequence #status predicted <sig> F):135-5140; Forduct: biliary glycoprotein 1, splice form a #status predicted <als: #status="" 1,="" 417-526="" 55-510="" 55-511;="" 55-519;="" <als:="" <irm:="" a="" and="" biliary="" brown="" d',="" domain:="" form="" glycoprotein="" gro<="" gross="" grows="" h',="" homology="" immunoglobulin="" predicted="" product:="" splice="" th="" x=""><th>Query Match 6.9%; Score 186; DB 1; Length 526; Best Local Similarity 21.5%; Pred. No. 4.2e-05; Matches 130; Conservative 80; Mismatches 200; Indels 196; Gaps 31; QY 5 LLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRODWTGSTPAX 57; Db 19 LLTASLLTFWNPTTAQLTTESMPRIANBGEKEVLLLVHNLEQQLE 63 QY 5 GK*WFKAVTTRGAPVATNHOSREVEMSTRGREVLIGDPAKG</th></als:></sig></sig>	Query Match 6.9%; Score 186; DB 1; Length 526; Best Local Similarity 21.5%; Pred. No. 4.2e-05; Matches 130; Conservative 80; Mismatches 200; Indels 196; Gaps 31; QY 5 LLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRODWTGSTPAX 57; Db 19 LLTASLLTFWNPTTAQLTTESMPRIANBGEKEVLLLVHNLEQQLE 63 QY 5 GK*WFKAVTTRGAPVATNHOSREVEMSTRGREVLIGDPAKG

Db 347 GGLGVVALL	C;Genetics: A;Gene: GDB:HSPG2 A;Cross-references: GDB:126372; OMIM:142461
· [1]	
489 GVRPRPEARMPK 50	us predicted
UD 388 1 USEEARMKE 390	
RESULT 15 A38096	325-359/Domain: LDL receptor ligand-binding repeat homology 368-403/Domain: LDL receptor ligand-binding repeat homology
perlecan precursor - human N;Alternate names: basement membrane heparan sulfate proteoglycan; heparan sulfate prote A:Graciae: Howe samione (man)	F;531-1676.Domain: ill <dom3> F;1159-1206.Domain: laminin-type EGF-like homology <leg> F:1563-1610.Domain: laminin-type EGF-like homology <eg7></eg7></leg></dom3>
C. Decree 07-Apr 1994 #sequence revision 07-Apr-1994 #text_change 12-Jul-2004 C.Accession: A38056; S19256; S77946; A41059; A40306; B33625; A33625; A41736	1613-1668/Domain: laminin-type EGF-like homology <
R;Murdoch, A.D.; Dodge, G.R.; Cohen, I.; Tuan, R.S.; Iozzo, R.V. J. Biol. Chem. 267, 8544-8557, 1992	;2007-2034/Domain: transmembrane;3687-4391/Domain: V <dom5></dom5>
A,Title: Primary structure of the human heparan sulfate proteoglycan from basement membr tor, laminin, neural cell adhesion molecules, and epidermal growth factor.	
AjAccesion: A38036 AjAocession: A38036 AjMolecule type: mRNA	
A, Residues: 1-4391 <mur> A; Residues: 1-4391 <mur> A; Cross references: UNIPROT: P98160; GB: M85289; NID: 9184426; PIDN: AAB52700.1; PID: 9184427</mur></mur>	74299-4301/Region: motor neuron attachment (L-K-E) 765,71,76/Binding site; heparan sulfate (Ser) (Cov.
•	:89,554,1/55,2121,30/2,3105,32/3,2/50,3636,4066/Binding Sire: Calbonydrade (Asir);2995,3933,4179/Binding sire: chondroitin sulfate (Ser) (covalent) #status predic
A:Title: Human basement membrane heparan sulfate proteoglycan core protein: a 467-kD protein adhesion molecules, and epidermal growth factor. A:Reference number: A4734; MITD:92112994; PMID:1730758	Query Match 6.7%; Score 180; DB 2; Length 4391; Best Local Similarity 20.4%; Pred. No. 0.0015;
A, Accession: S19256 A. Molecule trope: mBNa	nes 129; Conservative 68;
A,Residues: 1-57, 'D',59-434,'A',436,'FL',438-449,'Q',451-502,'A',503-792,'K',794-908,'R' 71-297,'H',5981-294,'G',596-3167,'T',3169-3240,'R',3242-3426,'R',3428-3631,'Q',3633-3 3. Cross-reference: PMBI.XFORIE	Qy 18 DGRFWIRVQESUMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW 60 11
Rituggsason, K.	Datswayaasohnravaantramyaxa
Budmitted to the Embi Data Albialy, Octobel 1991 A; Reference number: 8. Brosesion, 977946	3172 ISSAKPSDAGTYVCLAONALGTAOKOVEVIVDTGAMAPGAPOVOAEEAELTVEAGHTATL
	68
, , 363	3232 RCSATGSPAPTIHWSKLRSPLPWQHR
×	PGQPVTVICVENWAFBECPPP
A;Title: Cloning of human heparan sulfate proteoglycan core protein, assignment of the g A;Reference number: A41059; MUID:92120660; PMID:1685141	Db 3281 ISPAGHAEATIILHVESPPYATIVPEHASVQAGETVQLQCLAHGTPPLIFQWSRVG 3336
A/Accession: A41059 A/Molecule type: mRNA » Boaciding: 'PT' 000_000 'P' 010_1101 'I'' 1102_1139 'I'' 1134_1091 'I'' 1993_1397 'KB9.	Qy 185 LSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDL-VI 243
	Db 3337 SSLPGRATARNELLHFERAAPEDSGRYRCRVTNKVGSAEAFAQLLVQGPPGSLPAT 3392
	244 SISRDNTPDPPENLRVWVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPAR
A;Reference number: A40306; MUD:91365376; PMID:1679749 A;Accession: A40306	3393 SIPAGSTPTVQVTPQLETKSIGASVEFHCAVPSDQGTQ
A; Molecule type: mRNA A; Residues: 1018-1405, (3',1407-1409, 'G',1411-1465 < DOD>	OY 300 LSWTQRCQVLSFSQPSDPGVLELPRVQVEHEGERTTCHARHPLGSQHVSLSLSVHYKKGLI 359 A 21 1.DWFKFGCOLDGHRVQNGVIRTONDOSCOTTYTCOAHGWGKADASAQLVIOALDSVL 3490
A; LIOSE-TETELEMICES: GB: MOG-1833; NID: G18444; FIDN: AAA32093.1; FID: G104443 R; Heremans, A.; van der Schueren. B.; De Cock, B.; Paulsson, M.; Cassiman, J.J.; van den J. Cell Biol. 109, 3199-3211. 1989	360 STAFSNGAFLGITALLFLCLALIIMKILPKRRTQTETPRPRFS
A,Title: Matrix-associated heparan sulfate proteoglycan: core protein-specific monoclona anes.	3491
A;Reference number: A33625, MUID:90078352; PMID:2687294 A;Accession: B33625	Qy 405RHSTILDYINVVPTAGPLAGKRNQKATPNSPRTP 438
A;Molecule type: protein A;Residues: 1379-1384,'X',1386-1388,'X',1390-1398 <he2></he2>	Db 3537 GGVVRIAHVELADAGQYRCTATNAAGTTQSHVLLLVQALPQISMPQEVRVPAGSAAVFPC 3596
A;Recistor: A3-05-6 A;Residues: 2166-2171,'X',2173-2175,'X',2177-2185 <he3></he3>	439 LPPGAPSPESKKNOKKOYOLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPR
A,Note: peptide potentially matches four different regions of sequence shown	Db 3597 IASGYPTPDISWS-KLDGSLPPDSRLENNMLMLPSVRPQDAGTY 3639

Search completed: November 5, 2004, 13:51:01

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November 5, 2004, 13:50:17; Search time 59.6073 Seconds (without alignments) 3081.324 Million cell updates/sec
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ALIGNMENTS

RESULT 1

Human obesity protein binding protein-2 homologue; hOB-BP2h; obesity; obesity,related disorder; therapy. Human obesity protein binding protein-2 homologue #1. AAY97542 standard; protein; 512 AA (first entry) 12-FEB-2001 AAY97542; AAY97542

WO200059942-A2. Homo sapiens. 12-OCT-2000.

22-MAR-2000; 2000WO-US006682 02-APR-1999; 99US-0127667P.

WPI; 2000-664992/64. N-PSDB; AAA37847. Wei J; Su EW,

(ELIL) LILLY & CO ELI.

New human obesity protein binding protein-2 homologue nucleic acids, polynucleotides and polypeptides useful for producing medicament for treating obesity and/or obesity-related disorders.

Claim 9; Page 86-88; 92pp; English.

This sequence is a human obesity protein binding protein-2 homologue (hOB-BP2h) of the invention. The hOB-BP2h nucleic acids and polypeptides may be used for the manufacture of a medicament for the treatment of obesity and/or obesity-related disorders. The hOB-BP2h nucleic acids are useful as probes or amplification primers in the detection, quantification or isolation of gene sequences or transcripts, for recombinant expression of hOB-BP2h polypeptides, as immunogens in the preparation and screening of antibodies, and in sense or antisense suppression of one or more hOB-BP2h genes or nucleic acids, host cell or tissue in vivo or in vitro. Antigenic epitope-bearing peptides and polypeptides are useful for raising or screening antibodies that specifically binds to the hOB-BP2h polypeptides.

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120

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180 240 300

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420

180

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PLAQKRNOKATPNSPRTPLPPGAPSPESKKNOKKQYQLPSFPEPKSSTQAPESQESQEEL 480
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                                                                                                                                                                      PKAVTETTKGAPVATNHQSREVEMSTRGRPQLTGDPAKGNCSLVIRDAQMQDESQYFPRV
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                                                                                                                                                                                                                                                                                                             TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
                                                                                                                                                                                                                                                                                                                                         181 IGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
                                                                                                                                                                                                                                                                                                                                                                                 LVISISRDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPARL
                                                                                                                                                                                                                                                                                                                                                                                                                   241 LVISISRDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPARL
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                                                                                                  1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
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                                                                  Gaps
                                                                  ..
                               Length 512;
                                                                Indels
                               Score 2706; DB 3;
Pred. No. 2.8e-205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYATLNFPGVRPRPEARMPKGTQADYAEVKFQ 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYATLNFPGVRPRPEARMPKGTQADYAEVKFQ 512
                                                                0; Mismatches
                               100.0%;
                                                                Conservative
                                              Best Local Similarity
Matches 512, Conserv
Sequence 512 AA;
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AAUS7087

AAU87087 standard; protein; AAU87087;

05-JUN-2002

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Sialic acid-binding Ig-related lectin, Siglec-BMS-L3-995-3

immune system disease; leukaēmia; allergy; inflammatory disease; tissue damage; allergic rhinitis; osteoarthritis; Crohn's disease; psoriasis; rheumatoid arthritis; conjunctivitis. Human; sialic acid-binding Ig-related lectin; SIGLEC; asthma;

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sapiens Synthetic

WO200208257-A2

31-JAN-2002

20-JUL-2001; 2001WO-US023082

(BRIM) BRISTOL-MYERS SQUIBB CO 21-JUL-2000;

Whitney G; Chang H, Longphre M,

355

The invention relates to an isolated SIGLEC (Gialic acid-binding Igrelated lectin) protein (I). Pharmaceutical compositions comprising (I) related lectin) protein (I). Pharmaceutical compositions comprising (I) are useful for treating immunes system diseases such as asthma, leukaemia or or other allergic or inflammatory diseases. Extracellular domains of (I) to assays, and imaging methods. (I) is useful as a target for drugs which inflammatory diseases such as allergic remodeling in asthma, and cinflammation, tissue damage and remodeling in asthma, and cinflammatory diseases such as allergic rhinitis, osteoarthritis, Crohn's disease, psoriasis, rheumatoid arthritis, conjunctivitis, etc. (I) is also useful for monitoring the course of disease or disorders, and for identifying agents that bind with and/or modulate the biological activity of SIGLEC-BMS proteins. The nucleic acid molecules (II) encoding (I) are useful in diagnosis and/or prognosis methods, and to detect the presence and/or amount of SIGLEC-BMS uncleotide sequences and/or SIGLEC-BMS uncleotide sequences and/or signed probes are useful for screening genomic library to isolate a genomic clone of SIGLEC-BMS sortions of under is determined for detecting diseases or disorders associated with SIGLEC-BMS transcripts or proteins. The SIGLEC-BMS proteins and in diagnostic imaging technology.

ANURTONA-AAURTONA-AAURTONBY represent human SIGLEC amino acid sequences of the Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein molecules useful for treating immune system diseases such as asthma, leukemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease. Example 11; Fig 6; 209pp; English WPI; 2002-241565/29. N-PSDB; ABK43373.

Sequence 697 AA;

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480

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120 180 240 240 120 180 241 İVİSİSRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP 300 420 GEFTCHARHPLGSOHVSLSLSVHYSPKLLGPSCSWEAEGLHCSCSSQASPAPSLRWWLGE 480 ---K 355 9 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV ERGSYVRYNPMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW ERGSYVRYNPWNDGFFLKVTALIQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW TGAALSSQGTKPTTSHFSVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD ------PPENLRVMVSQANRTVLE NIGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE 1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRODWTGSTPAYGYW 1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRODWIGSTPAYGYW 61 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD WGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLE NIGNGTSLPVLEGGSLCLVCVTHSSPPARLSWTQRCQVLSPSQPSDPGVLELPRVQVEHE Indels 185; 95.4%; Score 2580.5; DB 5; Length 697; 73.2%; Pred. No. 3.6e-195; tive 1; Mismatches 1; Indels 185; GEFTCHARHPLGSQHVSLSLSVHY Conservative LVISISRDNTPD---Best Local Similarity Matches 510; Conserv 301 121 121 181 181 241 253 271 361 331 421 Query Match

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The invention relates to an isolated nucleic molecule that is at least 95% identical to 18 human cDNA sequences representing 12 novel genes encoding secreted proteins or a polynucleotide fragment of the cDNA sequence contained in American Type Culture Collection (ATCC) deposit No. defined in the specification, its species homologue, a variant or allelic
                        415
                                                                           475
                                                 900
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ELLEGNSSODSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAOSGSILQLPDK 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human secreted nucleic acid molecules and polypeptides, useful for preventing, treating, or ameliorating a medical condition, such as cancer, inflammation, immune disorders, neurological and blood clotting
                                                                                          KGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINV
                                           KGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINV
                                                                         VPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPESQE
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                                                                                                                                                                                                                                                                                                                      cytostatic, antiinflammatory, immunomodulator; neuroprotective; hemostatic; gene therapy, cancer; inflammation; immune disorder; neurological disorder; blood clotting disorder; food additive;
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                                                                                                                                                   661 SOEELHYATLNFPGVRPRPEARMPKGTOADYAEVKFO 697
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                                                                                                                                                                                                                                                                                                                                                               preservative; human; secreted protein
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                                                                                                                                                                                                                   ADA27153 standard; protein; 697
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27-CCT-1999; 99WO-US025031.
19-APR-2000; 2000US-0194792P.
30-CCT-2000; 2000US-0243792P.
18-APR-2001; 2001US-00836353.
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Crocker P
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KENNY J J.
OLSEN H S.
MOORE P A.
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CROCKER P 1
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M, Liu D,
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ADA27153
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the polymucleotide having a polymucleotide capable of does not hybridising under conditions the polymucleotide, where the polymucleotide does not hybridise under stringent conditions to a nucleic acid molecule having a nucleotide sequence of only A or T residues. Also included are recombinant vectors, host cells (for producing the polypeptide), the secreted polypeptide (comprising a sequence that is at least 95% identical to a polypeptide fragment, domain, epitope, full-length protein, variant, allelic variant or species homologue), antibodies that specifically bind to the polypeptides, diagnosing, treating, preventing or amelicrating a medical condition by administering the polymucleotide or the polypeptide, the gene corresponding to the CDNA sequence and identifying an activity in a biological assay dud detecting the supernatant, and detecting an activity or a polypeptides, nucleic acids and antibodies are useful for diagnosing a pathological condition, for preventing, treating, or amelicrating a medical condition, for preventing, treating, or amelicrating a custom as public acids and antibodies are disorders, neurological and blood clotting disorders (many examples are corresponding immunological probes for differential identification of the formy providing immunological probes for differential identification of the cissues immunological probes for differential identification of the tissues immunological probes for differential identification of the cissues immunological probes for differential identification of the cissues immunological probes for differential identification of the cissues immunological probes and anibodies are useful for increase or decrease storage capabilities, fat content or other manning immunological probes for differential identification of the increase or decrease storage capabilities, fat content or other increase or decrease storage capabilities, fat content or other increase.
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Pred. No. 7.4e-195;
1; Mismatches 2; Indels 185;
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Matches 509, Conservative
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416 VPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPESQE 475
541 KGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINV 600
                                                                                                              601 VPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPESQE
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                                                                                                                                                                                          SQEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ 512
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                                                                                                                                                                                                                                                                                                                                                                                                                      ADD26582 standard; protein; 697 AA
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The present invention describes human cell surface protein with immunoglobulin folds, designated BGS-19 (1). (1) has cytostatic, gynaecological, immunosuppressive, antinilammatory, antiasthmatic, antidiabetic and dermatological activities, and can be used in gene therapy. (1) can be used for preventing, treating or ameliorating a medical condition, such as a disorder related to aberrant immunoglobulin cell surface receptor activity, a cellular adhesion disorder; a disorder related to aberrant signal transduction; a reproductive disorder related to byper- or hypo-immunoglobulin receptor activity; a disorder related to byper or hypo-immunoglobulin receptor activity; a disorder related to aberrant signal transduction; a reproductive disorder; dysfunctional uterine bleeding; amenorrhoea; primary dysmenorrhoea; exual dysfunction; interility; pelvic inflammatory disease; endometriosis; placental aromanase deficiency; premature menopause; placental dysfunction; hormone deficiency; oestrogen deficiency; aberrant aberrant ovarian cycle; menorrhagia; metrorrhagia; menometrorrhagia; dysmenorrhoea; hypomenorrhoea; polymenorrhoea; dysfunctional uterine bleeding; resistant-ovary syndrome; hermaphroditism; immune disorders; inflammatory disorders; arthritis; asthma; immunodeficiency diseases such as AIDS; leukaemia; rheumatoia arthritis; granulomatous disease; inflammatory bowel disease; sepsis; acne; neutropenia; neutrophilia; androgen metabolism; aberrant onset of female puberty; aberrant showing of female primary sexual characteristics; aberrant showing of female secondary sexual characteristics; precocious puberty; precocious peeudopuberty; incomplete isosexual precocity; premature thelarche; New isolated nucleic acid molecule encoding BGS-19 polypeptides, useful for preventing, treating or ameliorating a medical condition, such as a disorder related to aberrant immunoglobulin cell surface receptor remature adrenarche; premature pubarche; polycystic ovarian disease; Example 1; SEQ ID NO 7; 224pp; English. activity

RESULT 5 ADI37010

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psoriasis; hypersensitivities; such as T-cell mediated cytotoxicity; immune reactions to transplanted organs and tissues; such as host-versus; graft and graft-versus; such as host-versus; catch and graft-versus; such as host-versus; catch and graft-versus; sold becase; near another infertility, Addison's Disease; hearnolytic anaemia; catchphalomyelitis; glomerulomephritis; dermatitis; allergic encephalomyelitis; glomerulomephritis; Goodpasture's Syndrome; Graves', Disease; Multiple Sclerosis; Mysthemia gravis; Neuritis; Ophthalmia; Disease; Multiple Sclerosis; Mysthemia gravis; Neuritis; Ophthalmia; Disease; Stiff-Wan Syndrome; autoimmune thyroiditis; Systemic Lupus Erythematosus; Autoimmune Pulmonary Inflammation, Guillain-Barre Syndrome; insulin dependent diabetes mellitus; autoimmune inflammatory eye disease; lens tissue injury; demyelination; systemic lupus erythematosus drug induced haemolytic anaemia; rheumatoid arthritis; Sjogren's disease and scleroderma. The present sequence is given in comparison with BGS-19; in the present invention.	7; Length ; Indels	VPCSFSYPRQ VPCSFSYPRQ	AKGNCSLVIRDA(AKGNCSLVIRDA(PVTVICVENWAFI	SRKGVS SRKGVS	SQPPATL	PPENLRVMVS 	LSPSQPSDPG	GLHCSCSSQA		RTOTETPRPRF:	KQYQLPSFPEP1 	512 697
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                            TGAALSSQGTKPTTSHFSVLSFTPRPQDHNTDLTCHVDFSRKGVSVQRTVRLRVAYAPRD
TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
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                                                                                              241 LVISISRDNTPD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to novel nucleic acids encoding human PRO secreted and transmembrane proteins. Extracellular proteins play important roles in the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells (for example proliferation, migration or differentiation) is typically governed by information cereaived from other cells and the immediate environment. The information is often transmitted by secreted polypepides (for example mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides and hormones) which are received and interpreted by diverse cell receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor-ligand interactions. The current invention provides the amino acid sequences of novel human membrane bound receptors and proteins, along with the CDNA sequences encoding them. The novel proteins of the invention may have cytostatic activities through the stimulation of chondsorytes. The nucleic activities through the consecution in a mammal: In addition, they may be useful for measuring or detecting the expression of a tumour associated gene. The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 8; Length 697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schoenfeld J, Wood W,
                                                                                                                                                                                      human, PRO; membrane bound protein; membrane bound receptor; cell proliferation; cell migration; cell differentiation; mitogenic factor; survival factor; cytotoxaic factor; addifferentiation factor; neuropeptide; hormone; cell receptor; receptor-ligand interaction; cytostatic; chondrocyte; tumour.
                                                                                                                                               Novel human secreted and transmembrane protein PRO 71236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.2%; Score 2576.5; DB 8; 73.0%; Pred. No. 7.4e-195; iive 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 10; SEQ ID NO 10; 118pp; English.
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  ADI37010 standard; protein; 697
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                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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Claim 10; Fig 7; 695pp; English.

The present invention relates to PRO proteins and their coding sequences.
The PRO proteins are useful for diagnosing and treating a B cell related disorder, eg. X-linked infentile hypogammaglobulinemia, polygacdharide antigen unresponsiveness, selective IgA deficiency, selective IgA deficiency, selective IgA deficiency, Burkitt's immunodeficiency with hypogammaglobulinemia of infancy, Burkitt's immunodeficiency with hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic anamia, mysthenia gravis, hypoadrenocorticism, glomerulomephritis, or anamia, mysthenia gravis, hypoadrenocorticism, glomerulomephritis, or anamylosing spondylitis. The PRO proteins are also useful for preparing a medicament for treating a condition that is responsive to the PRO proteins, e.g. cancer or immune-mediated inflammatory diseases. The PRO coding sequences are useful as hybridization probes in chromosome and gene mapping, in preparing PRO proteins, or in generating transgenic animals or knockout animals, which in turn are useful in the development and screening of therapeutically useful reagents.

Sequence 697 AA;

ä 240 252 270 900 FKAVTETTKGAPVAINHQSREVEMSTRGRFQLIGDPAKGNCSLVIRDAQMQDESQYFFRV 120 61 FKAVTETTKGAPVATNHQSREVEMSTRGREQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120 ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPBTLEPGQPVTVICVFNWAFEECPPPSFSW 180 121 ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW 180 301 WGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVWVSQANRTVLE 360 271 NLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE 330 361 NLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE 420 354 356 KGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINV 415 601 VPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPESQE 660 9 9 1 MILPLILSSILGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW 181 TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 241 LVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP 253 ------PPENERVMVSQANRTVLE 481 ELLEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQSGSILQLPDK 541 KGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINV 416 VPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPESQE Gaps Indels 185; 95.2%; Score 2576.5; DB 8; Length 697; 73.0%; Pred. No. 7.4e-195; ive 1; Mismatches 2; Indels 185; 331 GEFTCHARHPLGSQHVSLSLSVHY-------241 LVISISRDNTPD------Query Match Best Local Similarity 73.0 61 121 355

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diseases.

New isolated nucleic acids encoding signal transduction pathway component polypeptides, useful for diagnosing, treating, and/or preventing disorders, such as cancer, infections, cardiovascular and inflammatory human secreted protein, cytostatic; antibacterial; virucide; neuroprotective; gynaecological; gastrointestinal-Gen; cardiant; cardiavascular-Gen; nephrotropic; antibinflammatory; muscular-Gen; respiratory-Gen; immunosuppressive; cerebroprotective; vasotropic; neotropic; antiallergic; cancer; bacterial infection; viral infection; neural disorder; immune system disorder; blood disorder; miscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder; inflammatory disorder; proliferative disorder; human. Human secreted protein from gene 18 #3. ADD19314 standard; protein; 710 AA. 07-NOV-2001; 2001US-0331046P. (HUMA-) HUMAN GENOME SCI INC. 06-NOV-2002; 2002WO-US035606 (first entry) Rosen CA, Ruben SM; WPI; 2003-533050/50. N-PSDB; ADD19239 WO2003052377-A2. Homo sapiens. 15-JAN-2004 26-JUN-2003. ADD19314; RESULT 7 ADD19314

The invention relates to an isolated mucleo, actor mousecule (prower) concoding a human secreted protein, representing one of 85 novel genes. Also included are recombinant vectors, host cells (expressing the protein), the secreted proteins (including their fragments, epitopes and homologues), an isolated antibody that binds specifically to the protein, diagnosing a pathological condition or susceptibility to a pathological condition based on the presence or absence of a mutation in the mucleic acid and diagnosing a condition based on the presence or amount of expression of the protein in a biological sample and diagnosing a condition of comprising determining the presence or amount of expression of the protein in a biological sample and diagnosing a condition based on the presence or amount of expression of the protein in a biological sample and diagnosing a condition based on the presence or amount of expression of the protein in a biological sample and diagnosing a condition based on the presence or amount of expression of the protein in a biological sample of the protein, preventing, treating or ameliorating a medical condition by administering the nucleic acid or protein, the gene corresponding to the protein in the supernatant thaving the activity in a biological assay (comprising expressing the nucleic acid in a cell, isolating the special or protein and proteins display the following activities Cytostatic, antibacterial, virucide, Neuroprotective, Gynaecological, Gastrointestinal-Gen, Respiratory-Gen, Immunosuppressive, Gerebroprotective, Vasotropic, Cerebroprotective, The methods and compositions of the present prognosticating disorders related to the novel polypeptides, such as prognosticating disorders related to the novel polypeptides, such as prognedial or viral infections, and neural, immune system, blood, The invention relates to an isolated nucleic acid molecule (CDNA) Claim 11; SEQ ID NO 141; 554pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQH 345
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 muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, inflammatory or proliferative disorders (many examples of these diseases and disorders are given in the specification). The present sequence represents a novel secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLENLGNGTSLPVLEGQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          389 LCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQH
                                                                                                                                                                                                   29 GYGWEILDTSAGVSDGAGGLCISVPCSFSYPRODWTGSTPAYGYWFKAVTETTKGAPVAT
                                                                                                                                                                                                                                                                                              136 FLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSWTGAALSSQGTKPTTS
                                                                                                                                                                                                                                                                                                                                                                                     209 HFSVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLKVAYAPRDLVISISRDNTPALEP
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                                                                                                                                                                       19 GRFWIRVQESVMVPE---GLCISVPCSFSYPRQDWTGSTPAYGYWFKAVTETTKGAPVAT
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                                                                                                                                                                                                                                                        89 NHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRVERGSYVRYNFMNDGF
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                                                                                                                                           Gaps
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                                                                                                                                        10; Indels 188;
                                                                                                            Length 710;
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                                                                                                          Score 2417; DB 7;
Pred. No. 3.2e-182;
                                                                                                                                        3; Mismatches
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                                                                                                          89.3%;
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tissue
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The invention relates to an isolated SIGLEC (sialic acid-binding Igrelated lectin) protein (I). Pharmaceutical compositions comprising (I) are useful for treating immune system diseases such as asthma, leuksemia or other allergic or inflammatory diseases. Extracellular domains of (I) represent potential markers for screening, diagnosis, prognosis, follow-up dasasys, and imaging methods. (I) is useful as a target for drugs which inhibit inflammation, tissue damage and remodeling in astarget for drugs which inflammatory diseases such as allergic rinnitis, osteoarthritis, crohn's disease, psoriasis, rheumatorid arthritis, conjunctivitis, crohn's disease, psoriasis, rheumatorid arthritis, conjunctivitis, etc. (I) is also useful for monitoring the course of disease or disorders, and for identifying agents that bind with and/or modulate the biological activity of SIGLEC-BMS proteins. The nucleic acid molecules (II) encoding (I) are useful in diagnosis and/or prognosis methods, and to detect the presence and/or amount of SIGLEC-BMS nucleocide sequences and/or SIGLEC-BMS proteins in a biological sample. (II) are useful as nucleic acid probes are useful for screening genomic library to isolate a genomic clone of SIGLEC gene. SIGLEC-BMS antibodies are also used to detecting or proteins. The SIGLEC-BMS such object is determined for detecting expressing SIGLEC-BMS proteins and in diagnostic imaging technology.

AAUSTORY-AAUSTORY PARUSTORY human SIGLEC amino acid sequences of the
                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein molecules useful for treating immune system diseases such as asthma, leukemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease.
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al Similarity 75.1%; Pred. No. 2.2e-171;
452; Conservative 1; Mismatches 1;
psoriasis; rheumatoid arthritis; conjunctivitis.
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                                                                                                                                                                                                                                                    (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Fig 2B; 209pp; English.
                                                                                                                                                                      20-JUL-2001; 2001WO-US023082.
                                                                                                                                                                                                              21-JUL-2000; 2000US-0220139P.
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                                                                                   40200208257-A2
                                                                                                                                                                                                                                                                                                 Congphre M,
                                                                                                                             31-JAN-2002
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New secreted and transmembrane polypeptides and their polynucleotides, useful for treating blood coagulation disorders, cancers and cellular
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                                                    98US-0080333P

98US-0080333P

98US-0081049P

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98US-0081195P

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98US-0087208P
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N-PSDB; AAZ34109.
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                                                                              243 WGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLE 302
                                                                                                                                              331 GEFTCHARHPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILP 390
                                                                                                                                                                 422
                                                                                                                                                                                                423 KRRIQIETPRPRFSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAFSPESKK 482
                                                                                                                                                                                                                          NOKKOYOLPSFPEPKSSTQAPESQESQEBLHYATLNFPGVRPRPEARMPKGTQADYAEVK 510
                                                                                                                                                                                                                                        483 NQKKQYQLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK 542
                                                                                                                                                                                                                                                                                                                                                                                                               Ruman, PRO, BST; expressed sequence tag; PCR primer; hybridisation;
probe; blood coagulation disorder; cancer; cellular adhesion disorder;
secreted protein; transmembrane protein.
                                                                                                                  303 NLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHB
                                                                                                                                                           363 GEFTCHARHPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFTCLALIIMKKILP
                                                                                                                                                                                     KRRTQTETPRPRESRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPBSKK
                                                                                                        271 NLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE
                                                                                                                                                                                                                                                                                                                                      AAY41724 standard; protein; 544 AA.
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98US-0077641P.
98US-0077641P.
98US-00777641P.
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98US-0078916P.
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                                        The present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to oreate transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood cogulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AAZ33891 to AAZ34389, and AAX41685 to AAX41774 represent polynucleotide and polypeptide sequence given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                            61 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120
                                                                                                                                                                                                                                                                                                                           180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      303 NIGNGTSLPVLEGGSLCLVCVTKSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                        183 LVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                             3; Indels 148;
                                                                                                                                                                                       Length 544;
                                                                                                                                                                                       83.7%; Score 2265; DB 2;
74.8%; Pred. No. 2.4e-170;
ive 1; Mismatches 3;
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                     Claim 12; Fig 93; 530pp; English
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Matches 450; Conservative
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                                                                                                                                                                   Sequence 544 AA
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AAC78458 to AAC78599 represent polynucleotide and BST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bioactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bioactive molecules to cells. AAC78630 to AAC78837 represent PCR primers and probes used in the isolation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ľ,
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r H, Gerritsen ME;
L, Hillan KJ;
VF, Roy MA, Shelton D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel PRO polypeptides and polynucleotides used in detection methods, target bioactive molecules to specific cells, and to modulate cellular
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                                         Human, secreted protein; transmembrane protein; PRO; EST; cytostatic; expressed sequence tag; detection; cancer.
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Human PRO940 (UNQ477) protein sequence SEQ ID NO:259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.7%; Score 2265; DB 3;
74.8%; Pred. No. 2.4e-170;
live 1; Mismatches 3;
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99US-0123957P.
99US-01302432P.
99US-0131445P.
99US-0131445P.
99US-014569BP.
99US-014569BP.
99US-014569BP.
99WO-US028313.
99WO-US028313.
99WO-US028551.
99WO-US031244.
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Filvaroff E,
Godowski PJ,
Kuo SS, Napi,
Tumas D, Will
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N-PSDB; AAC78510.
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28. APR. 1999;
23. -UN. 1999;
26. -UL. 1999;
30. NOV 1999;
02. DEC. 1999;
02. DEC. 1999;
30. DEC. 1999;
30. DEC. 1999;
30. DEC. 1999;
30. DEC. 1999;
30. DEC. 1999;
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Goddard A, G
Kljavin IJ,
Stewart TA,
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29-MAR-1999
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                                                                              121 ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW 180
                                                                                                                                                                                                                            271 NLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE 330
                                                                                                                                                                                                                                                                331 GEFTCHARHPIGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILP 390
                                                                                                                                                                                                                                                                                                                    423 KRRTQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPPPPGAPSPESKK 482
                                                                                                                                                                                                                                                                                                                                      451 NQKKQYQLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK 510
                                                                                                                                                                                                                                                                                                                                                      483 NOKKOYOLPSFPEPKSSTQAPESQESGEELHYATINFPGVRPRPEARMPKGTQADYAEVK 542
                                                                                                                                                                                                                                           303 NLGNGTSLPVLEGGSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE
                                                                                                                 181 TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
                                                                                                                                  --------VLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
                                                                                                                                                                     183 ÍVÍSÍSRDNÍPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP
                                                                                                                                                                                                          243 WGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLE
                                                                                                                                                                                                                                                                               363 GEFTCHARHPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILP
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                                                  -----PPENLRVMVSQANRTVLE
                                                                                               121 ERGSYVTYNFMNDGFFLKVT---
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2000US-0198585P. 2000US-0199397P. 2000US-0199550P.

18-APR-2000; 25-APR-2000; 25-APR-2000;

2000US-0199654P 2000WO-US013705 2000WO-US014042

25-APR-2000; 03-MAY-2000; 17-MAY-2000; 22-MAY-2000;

2000US-0209832P 2000WO-US014941 2000WO-US015264

05-JUN-2000;

2000US-0196187P.

30-MAR-2000) 04-APR-2000) 04-APR-2000) 11-APR-2000) 11-APR-2000) 11-APR-2000) 11-APR-2000)

2000US-0196820P. 2000US-0198121P.

2000US-0194449P. 2000US-0194647P. 2000US-0195975P

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The PRO polypeptides and their associated nucleic acids can be used to rhe PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Wammals include dogs, cats, cattle, horses, sheep, pigs, goats mammal. Wammals include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adernal, hung, colon, breast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120
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                                                                                                                                                                                                                                                                                                                     PRO polypeptide; mammal; tumour; cancer; human; cattlo; horse; sheep; dog; cat; pig; goat; rabbit; tumour necroosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; colon; adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
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Gurney AL;

P, Chen J, Desnoyers L, Goddard A, Godowski PJ, Smith V, Watanabe CK, Wood WI, Zhang Z;

(GETH) GENENTECH INC.

Baker KP,

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Pan J,

01-DEC-2000; 20-DEC-2000;

24-AUG-2000

WPI; 2001-602746/68. N-PSDB; AAS45983.

Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumors, such as prostate and breast tumors, in mammals and screen for modulators of the compounds.

Claim 11; Fig 118; 774pp; English.

AAU29082 standard; protein; 544 AA.

Human PRO polypeptide sequence #59.

(first entry)

18-DEC-2001

AAU29082;

28-FEB-2001; 2001WO-US006520

WO200168848-A2. Homo sapiens.

20-SEP-2001

2000WO-US005601 2000WO-US005841 2000US-0186968P. 000US-0189320P 2000US-0189328P. 2000WO-US006884

01-MAR-2000;

2000US-0187202P

03-MAR-2000; 06-MAR-2000; 21-MAR-2000; 2000US-0190828P. 21-MAR-2000; 2000US-0191007P. 21-MAR-2000; 2000US-0191048P.

15-MAR-2000;

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10-JUN-1998;
11-OCT-1997;

13-NOV-1997;

24-NOV-1997;

24-NOV-1997;

11-DEC-1997;

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12-MAR-1998;

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02-JUN-1998;
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  NOKKOYQLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPRFBARMPKGTQADYAEVK 510
                                                       NLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDFGVLELPRVQVEHE 330
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                                                                                                                                            243 WGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLE 302
                                                                                                                                                                                                           GEFTCHARHPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILP 390
                                                                                                                                                                                                                     -----PPENLRVMVSQANRIVLE 270
 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120
                                                                                                                                                                                                                                                           LVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP
                    ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEFGQPVTVICVFNWAFEECPPPSFSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver; dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT; antibody-dependent enzyme mediated prodrug therapy.
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                                      ERGSYVTYNFWNDGFFLKVT----
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97US-0059266P.
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97US-0063120P.
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18-SEP-1997;
17-0CT-1997;
24-0CT-1997;
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28-0CT-1997;
29-0CT-1997;
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16-JUN-1998; 17-JUN-1998; 17-JUN-1998; 18-JUN-1998; 22-JUN-1998; 22-JUN-1998; 24-JUN-1998; 24-JUN-1998; 24-JUN-1998; 24-JUN-1998; 24-JUN-1998; 24-JUN-1998; 24-JUN-1998; 24-JUN-1998; 25-JUN-1998;

25-JUN-1998; 25-JUN-1998; 25-JUN-1998; 25-JUN-1998; 25-JUN-1998;

26-JUN-1998, 26-JUN-1998, 26-JUN-1998, 26-JUN-1998, 01-JUL-1998, 01-JUL-1998, 02-JUL-1998,

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FXAVTETTKGAPVATNHOSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQWQDESQYFRV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 LVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          363 GEFTCHARHPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILP
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Best Local Similarity 74.8%; Pred. No. 2.4e-170;
Matches 450; Conservative 1; Mismatches 3;
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  Human, secreted and transmembrane protein: PRO; gene therapy; tumour necrosis factor-alpha release; TNF-alpha release; chondrocyte proliferation; chondrocyte differentiation; tumour; adreanal tumour; lung tumour; colon tumour; breast tumour, prostate tumour; rectal tumour; cervical tumour; liver tumour.
                                                                                  Novel human secreted and transmembrane protein PR0940
               ABU88006 standard; protein; 544 AA
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NLGNGTSLPVLEGGSLCLVCVTHSSPPARLSWTORGQVLSPSQPSDPGVLELPRVQVEHE 330
                   --VLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 182
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                                                                                  ------PPENLRVMVSQANRTVLE
                                                                                               and transmembrane protein; PRO; TNF-alpha; factor alpha; chondrocyte cell; tumour; gene therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 ERGSYVRYNEMNDGFFLKYTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels 148; Gaps
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Pred. No. 2.4e-170;
1; Mismatches 3; Indels 14:
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Query Match Best Local Simil Matches 450; (

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Human; PRO; secreted protein; transmembrane protein; TNP-alpha; extracellular domain; tumour necrosis factor-alpha; TNP-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix; liver; drug screening; transgenic animal; genetic analysis; antiarthritic; vulnerary; gene therapy.
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larity 74.8%; Pred. No. 2.4e-170;
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³³¹ GEFTCHARHPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILP 390

³⁶³ GEFTCHARHPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILP 422

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Pred. No. 1e-177;
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) Publication No. US20030036631A1
) GENERAL INFORMATION:
) APPLICANT: LONGPART.
) APPLICANT: Chang Han
) APPLICANT: Chang Han
) APPLICANT: Chang Han
) TITLE OF INVENTION: NOVEL SIGLECS AND USES THE:
) FILE REFERENCE: DO003NP
) CURRENT APPLICATION NUMBER: US/09/910,600
) CURRENT APPLICATION NUMBER: 60/220,139
PRIOR PILING DATE: 2000-07-21
) NUMBER OF SEQ ID NOS: 32
) SOFTWARE: PATENTIN VET: 2.00
) SEQ ID NO 28

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1 MLDFLLLSSLLGGSQAMDGR......RPEARMPKGTQADYAEVKFQ 512
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/DSC NEW PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/USO NEW PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/USO NEW PUB.pep:*

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               GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-944-130-149
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US-09-910-600-8
US-09-978-255A-259
US-09-978-192A-259
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ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW
                                                          TGAALSSQGTKPTTSHESVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
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Pred. No. 2e-177;
1; Mismatches 2; Indels 185;
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FILE REFERENCE: PF489P2
CURRENT APPLICATION NUMBER: US/09/984,130
CURRENT FILING DATE: 2001-10-20
PRIOR PILING DATE: 2000-10-30
PRIOR PILING DATE: 2000-10-30
PRIOR PILING DATE: 2000-04-18
PRIOR PILING DATE: 2000-04-19
PRIOR PILING DATE: 2000-04-19
PRIOR FILING DATE: 1999-10-27
PRIOR FILING DATE: 1999-10-27
PRIOR FILING DATE: 1999-10-27
PRIOR FILING DATE: 1999-10-28
NUMBER OF SEQ ID NOS: 149
NUMBER OF SEQ ID NOS: 149
SEQ ID NO 149
SEQ ID NO 149
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"GE-10-403-938-7"

Sequence 7. Application US/10403938

Fublication No US20040025195A1

Fublication No US20040025195A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: NOVEL HUMAN CELL SURFACE PROTEIN WITH IMMUNOGLOBULIN FOLDS,

TITLE OF INVENTION: BGS-19

FILE REPRENCE: D0227 NP

FULE REPRENCE: D0227 NP

CURRENT APPLICATION NUMBER: U.S. 60/368,422

PRIOR APPLICATION NUMBER: U.S. 60/368,422

PRIOR PILING DATE: 2003-03-28

PRIOR PILING DATE: 2003-03-28

NUMBER OF SEQ ID NOS: 88

SOFTWARE: Patentin version 3.2
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US-10-403-938-7
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ORGANISM: Homo sapien
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US-10-614-853-10
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Sequence 10, Application US/10614853
FUDLICATION No. US20040138114A1
GENERAL INFORMATION:
JAPPLICANT: HENRY CHUU
JAPPLICANT: HILARY CHARK
JAPPLICANT: SHERMAN FONG
JAPPLICANT: SHERMAN FONG
JAPPLICANT: WILLIAM WOOD
JAPPLICANT: THOMAS WOUD
JAPPLICANT: WILLIAM WOOD
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JETTLE OF INVENTION: RELATED DISEASES
TITLE OF INVENTION: RELATED DISEASES
TITLE OF INVENTION: NUMBER: US/10/614,853
CURRENT APPLICATION NUMBER: US 60/394,485
PRIOR FILING DATE: 2002-07-08
NUMBER OF SEQ ID NOS: 28
NUMBER OF SEQ ID NOS: 28
JENGTH: 697
TYPE: PRT
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                                        1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
                                                                      FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
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              MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
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                                                                                                                        1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
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                                                                Gaps
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Pred. No. 2e-177;
1; Mismatches 2; Indels 185;
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APPLICANT: Chang, Han
APPLICANT: Chang, Han
APPLICANT: Chang, Han
APPLICANT: Mitney, Gena
TITLE OF INVENTION: NOVEL SIGLECS AND USES THEREOF
FILE REPRENCE: DO003NP
CURRENT APPLICATION NUMBER: US/09/910,600
CURRENT PILING DATE: 2001-07-20
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 32
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 8
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      Query Match
Best Local Similarity 73.0%;
Matches 509; Conservative
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APPLICATION NUMBER: 60/080194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 LVISISRDNIPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP 242
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                                                                                                                                                                                                                                                          1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
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                                                                                                                                                               148;
                                                                                                               84.2%; Score 2278; DB 10; Length 544; 75.1%; Pred. No. 5.3e-156;
                                                                                                                                                               Indels
                                                                                                                                                               1; Mismatches
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Grimaldi, J. Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ERGSYVRYNFMNDGFFLKVT-
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Filvaroff, Ellen
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Botstein, David
Desnoyers, Luc
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                                                                                                                                                                 Conservative
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                    TYPE: PRT ORGANISM: Homo sapiens S-09-910-600-8
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                                                                                                                                     Local Similarity
ses 452; Conserv
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US-09-978-295A-259
LENGTH: 544
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                                                                                                                 Query Match
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Matches
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LITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic RITLE OF INVENTION: Acids Encoding the Same
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APPLICATION NUMBER: 60/064249
FILING DATE: 1997-11-03
APPLICATION NUMBER: 60/065311
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APPLICATION NUMBER: 60/066364
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APPLICATION NUMBER: 60/079294
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APPLICATION NUMBER: 60/079923
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                                                                                                                                                                                                     Williams, P. Mickey
Wood, William I.
                                                                                                                                         Shelton, David L.
Stewart, Timothy A.
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FILING DATE: 1998-03-20
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llan, Kenneth
                     Ivar J.
                                                                                                 Nicholas
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                                                          Mary A.
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                                                                                                                       Margaret
                                                                                                                                                              Stewart, Timo
Tumas, Daniel
                                                                                                                                                                                                                                                                                    FILE REFERENCE: P2630P1C1
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KRRIQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKK 450
                                                                                  451 NOKKOYOLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK 510
                                      423 KRRIQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPPPPGAPSPESKK 482
                                                                                                                        483 NOKKQYQLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK 542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630PLC27 CURRENT APPLICATION NUMBER: US/09/978,697 CURRENT FILING DATE: 2001 10.1
                                                                                                                                                                                                                                                                                                                Sequence 259, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
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Gurney, Austin L.
Hillan, Kenneth J
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PRIOR FILING DATE: 2001-07-30
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PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
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APPLICATION NUMBER: 60/077641
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Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Napoleon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gerritsen, Mary E
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Botstein, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Margaret
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FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/078910
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APPLICATION NUMBER: 60/079786
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PLICATION NUMBER: 60/080165
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APPLICATION NUMBER: 60/079294
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APPLICATION NUMBER: 60/079689
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APPLICATION NUMBER: 60/079923
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APPLICATION NUMBER: 60/
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APPLICATION NUMBER: 60/
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APPLICATION NUMBER:
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1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW 1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW

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Matches

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61 FKAVTETTKGAPVATNHOSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV

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181 TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD

121 ERGSYVTYNFMNDGFFLKVT----

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1998-04-22 NUMBER: 60/082797 1998-04-23 NUMBER: 60/082796 1998-04-23 NUMBER: 60/08336 1998-04-28 1998-04-28 NUMBER: 60/08332 1998-04-28 NUMBER: 60/083392 1998-04-29 NUMBER: 60/083495 NUMBER: 60/083495 NUMBER: 60/083495	98-04-29 98-04-29 98-04-29 98-04-29 98-04-29 98-04-29 98-04-29 98-04-29 98-04-29 98-04-29 98-04-29 98-04-29 98-04-29 98-04-29 98-04-29 98-04-29 98-04-29 98-04-29 98-05-07 98-05-07 98-05-07 98-05-07 98-05-07 98-05-07 98-05-07 98-05-07 98-05-07 98-05-07 98-05-07 98-05-07 98-05-07 98-05-07 98-05-07 98-05-07	NUMBER: 60/084643 11998-05-07 11998-05-07 11998-05-13 11998-05-13 11998-05-13 11998-05-13 11998-05-13 11998-05-13 11998-05-15
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331 GEFTCHARHPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILP 390

363 GEFTCHARHPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILP 422

423 KRRIQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPPPPGAPSPESKK 482

KRRIQIEIPRPRESRHSTILDYINVVPTAGPLAQKRNQKATPNSPRIPLPPGAPSPESKK 450

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451

483 NOKKQYQLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK 542

FQ 544 FQ 512

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NOKKOYOLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK 510

303 NIGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDFGVLELPRVQVEHE 362

271 NLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE 330

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243 WGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLE 302

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183 LVISISRDNIPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP 242

Fong, Sherman Gao, Wei-Qiang Gerber, Hanspeter Gerritsen, Mary E. Goddard, Audrey Goddowski, Paul J. Grimaldi, J. Christopher Gurney, Austin L. Hillan, Kenneth J. Kljavin, Ivar J. RESULT 8
US-09-978-192A-259
Sequence 259, Application US/09978192A
; Patent No. US20020177553A1
; GENERAL INFORMATION: Ferrara, Napoleon Filvaroff, Ellen APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen APPLICANT: APPLICANT: APPLICANT: APPLICANT APPLICANT

Napier, Mary A. Pan, James; Paoni, Nicholas F.

Score 2265; DB 9; Length 544; Pred. No. 4.6e-155;

83.7%; 74.8%;

Query Match Best Local Similarity

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FILING DATE: 1998-04-09
APPLICATION NINBER: 60/081955
FILING DATE: 1998-04-15
APPLICATION NINBER: 60/081817
APPLICATION NINBER: 60/081817
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FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083545
                 FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/081070
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PLICATION NUMBER: 60/082568
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FILING DATE: 1998-04-22
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APPLICATION NUMBER: 60/083558
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FILING DATE: 1998-04-29
                                                                                   CATION NUMBER: 60/081049
                                                                                                       FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081071
                                                                                                                                                                                                                           APPLICATION NUMBER: 60/081203
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APPLICATION NUMBER: 60/082804
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APPLICATION NUMBER: 60/083322
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APPLICATION NUMBER: 60/083496
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APPLICATION NUMBER: 60/084640
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APPLICATION NUMBER: 60/0
FILING DATE: 1998-04-08
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                                                                FILING DATE: 1998-04-08
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APPLICATION NUMBER:
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APPLICATION NUMBER:
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APPLICATION NUMBER:
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                                                                                                                             TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same Fills OF INVENTION: Acids Encoding the Same CURRENT APPLICATION NUMBER: US/09/978,192A

CURRENT FILING DATE: 2001-10-15

PRIOR PELLING DATE: 2001-0-15

PRIOR PELLING DATE: 2001-0-15

PRIOR PAPLICATION NUMBER: 60/062250
                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-21
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APPLICATION NUMBER: 60/077450
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APPLICATION NUMBER: 60/077632
FILING DATE: 1998-03-11
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FILING DATE: 1998-03-13
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PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
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PRIOR APPLICATION WINBER: 60/079294
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PRIOR APPLICATION NUMBER: 60/079656
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FILING DATE: 1998-03-30
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PRIOR FILING DATE: 1998-03-11
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PLICATION NUMBER: 60/079664
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FILING DATE: 1998-03-27
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FILING DATE: 1998-04-01
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                                                                                      Williams, P. Mickey Wood, William I.
            nelton, David L.
Roy, Margaret Ann
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                                                                Tumas, Daniel
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CURRENT APPLICATION NUMBER: 05/0919.832A CURRENT FILING DATE: 2001-10-24
PRIOR FILING DATE: 2001-07-30
PRIOR FILING DATE: 1997-11-13
PRIOR PLICATION NUMBER: 60/06626
PRIOR PELING DATE: 1997-11-13
PRIOR PELING DATE: 1997-11-13
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                                                                                                                                                                                                                                                                   Sequence 259, Application US/09999832A Publication No. US20020192706A1 GENERAL INFORMATION:
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Grimaldi, J. Christopher
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Napter,
Pan, James;
Pani, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Eaton, Dan
APPLICANT: Fivaroff, Ellen
APPLICANT: Fivaroff, Ellen
APPLICANT: Fivaroff, Sherman
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Goddard, Audrey
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Kuo, Sophia S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Napier, Mary A.
                                                               511 FQ 512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      423 KRRIQIETPRPRPRPRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPPPPGAPSPESKK 482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 FXAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAXAPRD 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 LVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----VLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/08459
PRIOR APPLICATION NUMBER: 60/084600
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR FILING DATE: 1998-05-07
PRIOR FILING DATE: 1998-05-07
PRIOR PLING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/08433
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PRIOR PILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/08532
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PRIOR APPLICATION NUMBER: 60/08562
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83.7%; Score 2265; DB 9; Length 544;
Best Local Similarity 74.8%; Pred. No. 4.6e-155;
Matches 450; Conservative 1; Mismatches 3; Indels 14
APPLICATION NUMBER: 60/083496
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083499
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APPLICATION NUMBER: 60/084637
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APPLICATION NUMBER: 60/085339
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FILING DATE: 1998-04-29
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APPLICATION NUMBER: 60/08441
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TO THE PROPERTY AND ASSESSED TO THE PROPERTY OF THE PROPERTY O		1 FXAVIETIKGAPVAINHQSREVEMSTRGRFQLIGDPAKGNCSLVIRDAQMQDESQYFFRV	EKGSYVATYNEMNDGFFLKVIALIGKEDVIIFETLEFGGEVIVICVENNAFEECPPFSFSM ERGSYVTYNEMNDGFFLKVI	1 TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAXAPRD	1 LVISISRDNTPD		PPENLRVMVSQANRTVLE WGPRPLGLELPGVKAGDSGRYTCRAENRLGSOORALDLSVOYPPENLRVMVSOANRTVLE	NIGNGTSLPVLEQQSLCLVCVTHSSPPARLSWTCRQVLSPSQPSDFGVLELPRVQVEHE	NIGNGTSILPVLEGQSLCIVCVTHSSPPARISMTQRGQVLSPSQPSDPGVLELPRVQVEHE	1 GEFTCHARHPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILP 3 GEFTCHARHPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILP 3 GEFTCHARHPLGSOHVSLSSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILP 4	1 KRRIQTETFRPRFSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKK	3 KRRIQIETPRPRESRHSTILDYINVVPTAGPLAQKRNQKATPNSPRIPPPPGABSPKK	1 NOKKOYOLBSPPEPKSSTOAPESOBSOBELHYATLNFPGVRPRPBARMFKGTQADYAEVK	NOKKOYOLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK	FO 51	7. 2.	9 - 259	559, Application US/09978189 on No. US20030004102A1	FORMATION: : Ashkenati, Avi	: Baker Kevin P. Botstein, David : Besnovers Inc	: Eaton, Dan 2: Ferrara, Napoleon	Paroff, Bllen Paroff, Blen Paroff, Blen Paroff, Berman Paroff, Bretman Paroff,	?: Gao, Wei-Qiang ?: Gerber, Hanspeter	?: Gerritsen, Mary E. ?: Goddard, Audrey	F: Godowski, Paul J. F: Grimaldi, J. Christopher	Gurney, Austin L. F: Hillan, Kenneth J	R. Kljavin, Ivar J. R. Kuo, Sophia S.	Napier, Mary A. Pan, James,			F. Williams, P. Mickey F. Wood, William I. INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

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APPLICATION NUMBER: 60/084643 FILING DATE: 1998-05-07 FILING DATE: 1998-05-07 FILING DATE: 1998-05-07 FILING DATE: 1998-05-13 APPLICATION NUMBER: 60/08533 APPLICATION NUMBER: 60/08532 FILING DATE: 1998-05-13 FILING DATE: 1998-05-13 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/08550 APPLICATION NUMBER: 60/08569 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/08559 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/08559 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/08559 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/08553 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/08553 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/08553 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/08553 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/08553 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/08553 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/08554 APPLICATION NUMBER: 60/08557	Match Jocal Similarity 74.8%; Score 2265; DB 10; Length 544; Jocal Similarity 74.8%; Pred. No. 4.66-155; Be 450; Conservative 1; Mismatches 3; Indels 148; Gaps I MLIPLLISSLIGGSQAMDGRFWIRVDESVWVPEGLCISVPCSFSYPRODWTGSTPAYGYW 60		
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                                                                                                                                                           KRRIQIEIPRPRFSRHSTILDYINVVPTAGPLAQKRNQKAIPNSPRIPLPPGAPSPESKK 450
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271 NIGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE 330
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APPLICANT: Pan, James;
APPLICANT: Pan, James;
APPLICANT: Pan, James;
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypep
TITLE OF INVENTION: Acids Encoding the Same
FILE REPRENCE: P2630PLCLS
CURRENT APPLICATION NUMBER: US/09/978,585A
CURRENT PILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 624
Prior Application removed - See File Wrapper or Palm
SEQ ID NO 259
TYPE: DATE
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Pred. No. 4.6e-155;
1; Mismatches 3;
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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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ilarity 74.8%;
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Gerber, Hanspeter
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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ORGANISM: Homo sapiens
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APPLICANT: Williams P. Mickey
APPLICANT: Williams P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Scretced and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERBORS. D2630PLC22
CURRENT APPLICATION WUMBER: US/09/978,608A
CURRENT FILING DAIE: 2001-10-16
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Prior Application removed - See File Wrapper or Palm
SEQ ID NO 259
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
                                            Sequence 259, Application US/09978608A Publication No. US20030045462A1 GENERAL INFORMATION:
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Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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74.8%;
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Kuo, Sophia S.
                                                                                                   APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan
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Best Local Similarity 74.8
Matches 450; Conservative
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                                 61 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120
                                                                        ERGSYVRYNFWNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW 180
                                                                                                                                                                                ---VLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 182
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                                                                                                                                            181 TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
                                                                                                                                                                                                                                                        183 LVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP
                                                                                                                                                                                                                                                                                           -- PPENLRVMVSQANRTVLE
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                                                                                                         121 ERGSYVTYNFMNDGFFLKVT------
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APPLICANT: Ashkenazi, Avi
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Shelton, David L.
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Williams, P. Mickey
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Paoni, Nicholas F
Roy, Margaret Ann
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Filvaroff, Ellen
Fong, Sherman
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Desnoyers, Luc
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US-09-978-191A-259
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IIILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IIILE OF INVENTION: Acids Encoding the Same
                                                            FILE REPERENCE: P2630P1C4
CURRENT APPLICATION NUMBER: US/09/978,191A
                                                                                                                                             PRIOR FILING DATE: 2001-07-30
REIOR APPLICATION NUMBER: 60/062250
REIOR PILING DATE: 1997-10-17
REIOR PLING DATE: 1997-10-17
REIOR PLING DATE: 1997-11-03
REIOR PLING DATE: 1997-11-03
PRIOR PLING DATE: 1997-11-13
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                                                                                                        CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
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APPLICATION NUMBER: 60/077649
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FILING DATE: 1998-03-30
APPLICATION NUMBER: 60/080105
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APPLICATION NUMBER: 60/078886
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APPLICATION NUMBER: 60/079656
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APPLICATION NUMBER: 60/079689
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FILING DATE: 1998-03-31
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APPLICATION NUMBER: 60
Wood, William I.
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URRENT FILING DATE: 2002-03-19
nence 259, Application US/09978403A
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WRAL INFORMATION:
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Grimaldi, J. Christopher
Gurney, Austin L.
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helton, David L.
tewart, Timothy A
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                                                             PLICANT: Ashkenazi, Avi
PLICANT: Baker Kevin P.
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                                                                                                                                                                                                                                                                                         183 LVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP
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                                                                             TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Wood, William I.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Shelton, David L.
Stewart, Timothy A.
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Gerritsen, Mary E.
Goddard, Audrey
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Paoni, Nicholas F.
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Kuo, Sophia S.
Napier, Mary A.
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
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US-09-978-564A-259
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PRIOR FILING DATE: 1998-04-29
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Search completed: November 5, 2004, 14:13:46 Job time: 92.0765 secs

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OM protein - protein search, using sw model

November 5, 2004, 13:50:17; Search time 17.7654 Seconds (without alignments) 3460.797 Million cell updates/sec Run on:

US-09-937-636-4 3377 1 MLPPLLASSLIGGSQAMDGR.....RPEARMPKGTQADYAEVKFQ 639 Title: Perfect score: Sequence:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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11	82.	8.4	1694	~	S50065	sialoadhesin - mou
12	LΩ	7.6	4391	N	A38096	perlecan precursor
13			628	7	I38000	Lutheran blood gro
14	4,	7.3	647	N	A35648	-cell adhe
15	9 0		588	7	137202	protein -
16		7.0	761	₽	IJHUNG	adhe
17	ന		725	-	IJMSNG	cell
18	ന		858	Н	IJRINC	cell
19	m		1115	Н	IJMSNL	neural cell adhesi
20	31.	•	526	Н	A32164	biliary glycoprote
21	•		5175	7	T20992	hypothetical prote
22	26.	•	5198	7	T43290	hemicentin precurs
23	226	6.7	917	7	148950	phal
24	N		3707	N	S18252	9.7
25	N		4	(N	T37190	- human
26	α		S	H	IJBONC	cell
27	23.	9.9	811	N	4105	asciclin II, tra
28		٠	7	N	4	iclin II PI-I
29	18.	6.5	σ	-	IJCHNI	neural cell adhesi

19;

Gaps

Query Match
Best Local Similarity 23.9%; Pred. No. 2.4e-24;
Matches 169; Conservative 100; Mismatches 256; Indels 182;

transient axonal g	axonal glycoprotei	protein-tyrosine k	transmembrane carc	vascular cell adhe	connectin/titin -	biliary glycoprote	connectin 3B - chi	biliary glycoprote	carcinoembryonic a	elastic titin - hu	protein-tyrosine-p	pregnancy-specific	fasciclin II precu	neural cell adhesi	probable neural ce
449356	134695	JC4593	330127	JC2457	T42633	JC1509	PN0568	534338	436319	138346	TDFFLK	D33258	A40114	JN0635	T42718
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2 A4	2 A:	2 J	0	7	C)	7	0	α	Ø	~	-	0	7	н	c
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6.3 1040 2 /	6.2 1040 2 7	6.2 1070 2	6.1 464 2	6.1	0.9	201.5 6.0 458 2	6.0	5.9 521 2	5.9 702 2	5.9 7962 2	5.9 2029 1	8	5.8	196 5.8 1092 1	C PUCI R R R 201

ALIGNMENTS

21 FWIRVQESVMVPEGLCISVPCSFSYPRODWTGSTPAYGYWFKAVTETT 68	J. Cell Biol. 104, 957-965, 1987 A;Title: The amino acid sequences of the myelin-associated glycoproteins: homology to the A;Reference number: A27185; MUID:87166195; PMID:2435742
69 KGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDBSQYFFRVERGSYVRY 128	A;Accession: AZINBA A;Molecule type: mRNA A;Residues: 1-626 <sal> A;Crose-references: GB:X5301; NID:g56611; PIDN:CAA28920.1; PID:g56612</sal>
129 NFM	Kisuccinter, J.C.; Mainer, K.J.; Shinnick, I.M.; Bloom, F.B. Cell 133, 671-682, 1983 A;Title: Identifying the protein products of brain-specific genes with antibodies to offen A;Reference number: A90836; MUID:83259254; PMID:6347394
132NDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVISI 187 138 RLREDEGTWVQVSLLHFVPTREANGHRLGCQASFPNTTLQFEGYASMDVKYPPVIVEM 245	A;Accession: A90836 A;Molecule type: mRNA A;Residues: 'KS', 311-626 <sut> A;Cross-references: GB:V01544; GB:J00756; NID:g56879; PIDN:CAA24786.1; PID:g818027</sut>
188 SRDNTPALEPQPQGNVPYLEAQKGQPLRLLCAADSQPPATLSWVLQNRVLSSSHPWGPRP 247 1	A;Experimental source: clone p18236 A;Note: the authors translated the codon CAG for residue 350 as Asn R;Bloom, F.E.; Battenberg, E.L.F.; Milner, R.J.; Sutcliffe, J.G. J. Neurosci. 5, 1781-1802, 1985
248 LGLELPGVKAGDSGRYTCRAENRLGSQORALDLSVQYPPENLRVMVSQANRTVLENIGNG 307 288 LLLELEEVTPAEDGVYACLAENAYGQDNRTVGLSVMYAPWKPTVNG 333	A,Title: Immunocytochemical mapping of 18236, a brain-specific neuronal polypeptide degud A,Reference number: 156564, MUID:85263773, PMID:4020419 A,Accession: 156564 A,Status: preliminary, translated from GB/EMBL/DDBJ
308 TSLPVLEGGSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTC 367 334 TMVAV-EGETVSILCSTQSNPDPILTIFKEKQILSTVIYESELQLELPAVSPEDDGEYMC 392	A;Molecule type: mRNA A;Residues: 'KS',311-626 <res> A;Kresidues: 'KS',311-626 <res> A;Cross-references: CB:MJ6702; NID:g203181; PIDN:AAA40831.1; PID:g203182 R;Sutcliffe, J.G.; Milner, R.J.; Bloom, F.E.</res></res>
368 HARHPLGSQHVSLSLSVHYSPKLLGPS-CSWFABGLHCSCSSQASPAPSLRWWLGBELLE 426	Cold Spring Harb. Symp. Quant. Biol. 48, 477-484, 1983 A;Title: Cellular localization and function of the proteins encoded by brain-specificants A;Reference number: 152892; MUID:84206577; PMID:6586369 A;Accession: 152892
427 GNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAMNVHGAQSGSILQLPDKKGLI 486 453 VNESEREF-VYSERSGLVLTSILTLRGQAQAPPRVICTARNLYGAKSLELP 502	A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 'XS',311-626 <re2> A;Cross-references: GB:M11721; NID:g206780; PIDN:AAA42082.1; PID:g206781</re2>
487 STAFSNGAFLGIGITALLFLCLALIIMKILFKRRIQTBIPRPRFSRHSTILDYIN 541 503FQGAHRLMMAKIGPVGAVVAFAILIAIVCYITQTRRKKNVTESFSFS 549	C; Comment: The sequence contains five presumably extracellular domains that are digitable. C; Comment: The long form predominates in early postnatal life; alternative splicing-proof C; Comment: The papers cited variously predict the mature protein to begin at residue for C; Genetics:
542 VVETAGPLAQKRNQKATPNSPRTPLPPGAPSP-ESKKNQKKQYQLPSFPE 590 550AGDNPPVLFSSDFRISGAPEKYESERRLGSERRLGGL 586	A,Gene: MAG A,Map position: 7 C,Superfamily: myelin-associated glycoprotein; immunoglobulin homology C,Keywords: alternative splicing; brain; cell adhesion; duplication; glycoprotein; teans
591 PKSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK 637 1 1 1 1 1 1 1 1 1 1	F;1-19/Domain: signal sequence #status predicted <sig> F;20-626/Product: myelin-associated glycoprotein, long splice form #status predicted *MAG F;35-102/Domain: immunoglobulin homology <imm1.> F;135-120/Region: cell attachment (R-G-D) motif F;152-219/Domain: immunoglobulin homology <imm2.> F;254-307/Domain: immunoglobulin homology <imm3.></imm3.></imm2.></imm1.></sig>

myelin-associated glycoprotein precursor, long splice form - rat
NyAlternate names: 18256, brain neuron cytoplasmic protein 3; MAG
NyAlternate names: 18256, brain neuron cytoplasmic protein 3; MAG
C,Species: Rattus norvegicus (Norvay rat)
C,Date: 19-Feb-1984 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004
C,Date: 19-Feb-1984 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004
C,Bate: 19-Feb-1984 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004
R,Lai, C.; Brow, M.A.; Nave, K.A.; Noronha, A.B.; Quarles, R.H.; Bloom, F.E.; Milner, R.PECC. Natl. Acad. Sci. U.S.A. 84, 4337-4341, 1987
A,Title: Two forms of 18236/myelin-associated glycoprotein, a cell adhesion molecule for A,Reference number: A29028; MUID:87232001; PMID:2438699 A, Molecule type: mRNA
**Residues: 1-62 < LAL:
**Residues: 1-62 < LAL:
**A, Residues: 1-62 < LAL:
**A, Residues: 1-62 < LAL:
**A, Residues: 1-62 < LAL:
**A, Residues: 1-62 < LAL:
**A, Residues: 1-62 < LAL:
**A, Residues: 1-62 < LAL:
**A, Roder: J.; Chia, L.S.; Down, J.; Wilkinson, D.; Bayley, H.; Braun, P.; Du Roder: Natl. Acad. Sci. U.S.A. 84, 600-604, 1987
**A, Roder: Natl. Acad. Sci. U.S.A. 84, 600-604, 1987
**A, Reference number: A, Roder: Mulb: Roders; PMID: 2432614
**More ession: A94175; MUID: ROGES; PMID: 2432614 "Arcross-references: GB:M14871; NID:g205267; PIDN:AAA41556.1; PID:g205268 R. R. Salzer, J.L.; Holmes, W.P.; Colman, D.R. A Residues: 1-626 <ARQ> Almolecule type: mRNA

,Map position: 7 ;Superfamily: myelin-associated glycoprotein; immunoglobulin homology ;Superfamily: myelin-associated glycoprotein; cell adhesion; duplication; glycoprotein; transoc; ;1-19/Domain: signal sequence #status predicted <SIG> ;20-626/Product: myelin-associated glycoprotein, long splice form #status predicted *WM A;Experimental source: clone p18236
A;Note: the authors translated the codon CAG for residue 350 as Asn
R;Bloom, F.E.; Battenberg, B.L.F.; Milner, R.J.; Sutcliffe, J.G.
J. Neurosci. 5, 1781-1802, 1987
A;Title: Immunocytcochemical mapping of 18236, a brain-specific neuronal polypeptide dego
A;Reference number: 156564; MUID:85263773; PMID:4020419 R;Sutcliffe, J.G.; Milner, R.J.; Bloom, F.E.
Cold Spring Harb. Symp. Quant. Biol. 48, 477-484, 1983
Affile Cellular localization and function of the proteins encoded by brain-specificanien A;Reference number: I52892; MUID:84206577; PMID:6586369
A;Accession: I52892 Cross-references: GB:M11721; NID:g206780; PIDN:AAA42082.1; PID:g206781 ;Comment: The sequence contains five presumably extracellular domains that are dispublicated of comment: The long form predominates in early postnatal life; alternative splicited of comment: The papers cited variously predict the mature protein to begin at residue 10 131 132 ----NDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVISI 187 9 10 FWIMISASRGGHWGAWMPSSISAFEGTCVSIPCRFDFP--DELRPAVVHGVWYFNSPYPK 67 21 FWIRVQ-------ESVMVPEGLCISVPCSFSYPRODWTGSTPAYGYWFKAVTETT 69 KGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRVERGSYVRY 128 TFSEHSVLDIINTPNIVVPPEVVAGTEVBVSCMVPDNCPELRPELSWLGHEGLGEPTVLG A,Status: preliminary; translated from GB/EMBL/DDBJ A,Moleoule type: mRNA A,Residues: 'KS', 311-626 <RES> A,Cross-references: GB:M36702; NID:g203181; PIDN:AAA40831.1; PID:g203182 260; Indels 172; F,425-490/Domain: immunoglobulin nomology communo F,514-536/Domain: transmembrane #status predicted <TMM> F,514-626/Domain: intracellular #status predicted <INT> tch al Similarity 23.6%; Pred. No. 7.9e-24; 166; Conservative 104; Mismatches 260, A:Status: preliminary; translated from GB/EMBL/DDBJ A:Molecule type: mRNA A:Residues: 'KS', 311-626 <RE2> ,35-102/Domain: immunoglobulin homology <IMM1>,118-120/Region: cell attachment (R-G-D) motif :: 129 NFM---Accession: I56564 Query Match Best Local S Matches 166 Genetics: 엄 à à 셤 ద ò

√M.

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myelin-associated glycoprotein - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1990 #sequence revision 23-Mar-1990 #text_change 23-Jul-1999
C;Accession: B33785; A33785; So5687; SO257; So257; Sozius R.; Sakimura, K.; Inuzuka, T.; Takahashi, S
B;Pujita, N.; Sato, S.; Kurihara, T.; Kuwano, R.; Sakimura, K.; Inuzuka, T.; Takahashi, S
Biochem. Biophys. Res. Commun. 165, 1162-1169, 1989
A;Fitle: CDNA cloning of mouse myelin-associated glycoprotein: a novel alternative splic:
A;Reference number: A33785; MUD:90121220; PMID:2482022
A;Status: preliminary
                                                                                                                                                                                              (covalent) #status pred
  short splice form #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----NDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVISI 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLENLGNG 307
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                                                                                                                                                                                                                                                                                                                                                                                                                    69 KGAPVATNHOSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRVERGSYVRY
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                                                                                                                                                                                                                                                                                    Indels 129;
F;20-582/Product: myelin-associated glycoprotein, short splice form f;35-102/Domain: immunoglobulin homology <IMM1>
F;35-102/Domain: immunoglobulin homology <IMM2>
F;182-219/Domain: immunoglobulin homology <IMM2>
F;254-30/Domain: immunoglobulin homology <IMM3>
F;340-394/Domain: immunoglobulin homology <IMM4>
F;425-490/Domain: immunoglobulin homology <IMM4>
F;425-490/Domain: irmanoglobulin homology <IMM5>
F;514-536/Domain: transmembrane #startus predicted <ITM>F;537-582/Domain: intracellular #startus predicted <ITM7>
F;99,223,246,315,332,406,450,454/Binding site: carbohydrate (Asn)
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                                                                                                                                                                                                                                        13.9%; Score 469.5; DB 1; 24.7%; Pred. No. 3e-23; iive 89; Mismatches 226;
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Best Local Similarity 24.7
Matches 146; Conservative
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A;Residues: 1-637 < FUU>
A;Cross-references: GB:M31811
A;Accession: A33785
A;Status: preliminary
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NyAlternate names: 18236; brain neuron cytoplasmic protein 3; MAG
C;Species: Rattus norvegicus (Norway rat)
C;Botces: Rattus norvegicus (Norway rat)
C;Botces: Satus norvegicus (Norway rat)
C;Accession: B29028; B27185; Ā60055
R;Lai, C.; Brow, M.A.; Nave, K.A.; Noronha, A.B.; Quarles, R.H.; Bloom, F.E.; Milner, R.
R;Cital, C.; Brow, M.A.; Nave, K.A.; Noronha, A.B.; Quarles, R.H.; Bloom, F.E.; Milner, R.
R;Cital: Two forms of 1B236/myelin-associated glycoprotein, a cell adhesion molecule for A;Reference number: A29028; MUID:87232001; PMID:2438699
A;Residues: 1-582 C.AA.
A;Residues: 1-582 C.AA.
A;Cross-references: GB:M22357; NID:9205271; PIDN:AA41558.1; PID:9205272
R;Salzer, J.L.; Holmes, W.P.; Colman, D.R.
J; Cell Biol. 104, 957-965, 1987
A;Tile: The amino acid sequences of the myelin-associated glycoproteins: homology to the A;Reference number: A27185; MUID:87166195; PMID:2433742
A;Accession: B27185,
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;Keywords: alternative splicing; brain; cell adhesion; duplication; glycoprotein;
;1-19/Domain: signal sequence #status predicted <SIG>
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                                                                                                                                                                                                                                                                                                             HARHPLGSQHVSLSLSVHYSPKLLGPS-CSWEAEGLHCSCSSQASPAPSLRWWLGEELLE 426
    RIREDEGTWVQVSLLHFVPTREANGHRLGCQAAFPNTTLQFEGYASLDVKYPP--VIVEM 245
                                                SRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHPWGPRP 247
                                                                                                                                    LGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLENLGNG 307
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the long form predominates
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                                                                          GNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQSGSILQLPDKKGLI
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A; Residues: 419-582 <8AL>
A; Residues: 419-582 <8AL>
A; Cross-references: GB:X06554; NID:956614; PIDN:CAA29797.1; PID:91334302
R; Tropak, M.B.; Johnson, P.W.; Dunn, R.J.; Roder, J.C.
R; Tropak, M.B.; Johnson, P.W.; Dunn, R.J.; Roder, J.C.
A; Title: Differential splicing of MAG transcripts during CNS and PNS deve
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A,Molecule type: mRNA
A,Residues: 565-582 <TRO>
C,Comment: The sequence contains five )
C,Comment: The short form is found in it
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A; Cross-references: UNIPROT: P20138
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1988
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Best Local Similarity 21.3%;
Matches 148; Conservative
                                                                                                                                                             A, Residues: 1-364 <SIM>
                                                                                                                                    A; Molecule type: mRNA
                                                                                                 A; Accession: A30521
                                                                                                                                                                                                                                                               A; Gene: GDB:CD33
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                                                           Aftross-references: GB:M31811; NID:g199016; PIDN:AAA39487.1; PID:g199017
K. Fullta, N.; Sato, S.; Kurihara, T.; Inuzuka, T.; Takahashi, Y.; Miyatake, T.
R. Fullt. 232, 323-327, 1988
A. Title: Developmentally regulated alternative splicing of brain myelin-associated glyco
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13.8%; Score 466.5; DB 2;
Best Local Similarity 24.6%; Pred. No. 5.4e-23;
Matches 145; Conservative 91; Mismatches 225;
                                                                                                                                                                                                                                                           ")Molecule type: mRNA
A)Residues: 310-374,566-573,584-588 <FU2>
A)Cross-references: BMBL:X07849
                                                                                                                                                                                                                                                                                                                                                                                            Molecule type: mRNA
Residues: 310-374;566-582 <FU4>
Cross-references: BMBL:X07849
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                                                                                                                                                                                                                                                                                                                                                                    Accession: S02374
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A,Title: Isolation of a cDNA encoding CD33, a differentiation antigen of myeloid progention A,Reference number: A30521; MUID:89009814; PMID:3139766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||| :|:: : ||
BRGS-TXYSYKSPQLSVHVTDLTHRPKILIPGTLEPGHSKNLTCSVSWACEQGTPPIFSW 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 LSAAPTSLGPRTTHSSVLIITPRPQDHGTNLTCQVKFAGAGVTTERTIQLNVTYVP---- 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISISRDNTPALEPOPOGNVPYLEAOKGOFLRLLCAADSOPPATLSWVLONRVLSSSHPWG 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          245 PRPLGLELPGVKAGD-SGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLEN 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 LGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEG 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EFTCHARHPLGSQHVSLSLSVHYSPKLLGPSCSWEAEGLHCSCSSQASPAPSLRWWLGEE 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              424 LLEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQSGSILQLPDKK 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  484 GLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINVV 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --TETSSCSGAAPTVEM 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MPLLLLLPLLWAGALANDPNFWLQVQBSVTVQBGLCVLVPCTFFHPIPYYDKNSPVHGYW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPESQES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 364;
                                                                                                                                                                                                                                                                                                                                                               protein
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                                                                                                                                                                                                                                                                                A,Cross-references: GDB:119762; OMIM:159590
A;Map position: 19q13.3-19q13.4
C;Keywords: glycoprotein; surface antigen; transmembrane
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-259/Domain: extracellular #status predicted <EXT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;260-282/Domain: transmembrane #status predicted <TMV>F;283-364/Domain: intracellular #status predicted <CYT>F;100,113,160,209,230/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.4%; Score 451.5; DB 2;
21.3%; Pred. No. 2.6e-22;
live 49; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              335 DEELHYASLNFHGMNP----SKDTSTEYSEVRTQ 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              604 QEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ERGSYVRYNFMNDGFFLKVT-------
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A;Accession: 149583
A;Accession: 149583
A;Molecule type: mRMA
A;Molecule type: mRMA
A;Residues: 1-862 <RES>
A;Cross-references: UNIPROT:P35329; GB:L16928; NID:g348965; PIDN:AAA02562.1; PID:g348966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            574 GAMERWAL----GVKEGSGAP--QEVIPTSH------PPMKP----TKGPLEDPPBYAEIR 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                           m33-B isoform - mouse
C;Species: Mus sp. (mouse)
C;Species: Mus sp. (mouse)
C;Dacession: 1956 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: 152590
R;Tchilian, E.Z.; Beverley, P.C.; Young, B.D.; Watt, S.M.
Blood 83, 3188-3198, 1994
A;Title: Molecular cloning of two isoforms of the murine homolog of the myel A;Reference number: 152590; MUID:94250900; PMID:8193354
A;Accession: 152590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 149583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 MSTALTSLSSRTTDSSVLTFTPQPQPHGTKLTCLVTFSGAGVTVERTIQLNVTRKSGQMR
                                                                  --KKQYQLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MIMPLPLFLICAGSLAQDLEFQLVAPESVTVEEGLCVHVPCSVFYPSIKLT-LGPVTGSW
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21.5%; Pred. No. 1.2e-12;
Live 97; Mismatches 276; Indels 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.9%; Score 368; DB 2; 36.9%; Pred. No. 8.7e-17; iive 22; Mismatches 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-403 <RES>
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240 ELVL 243
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A; Residues: 1-620 <br/>
A; Residues: 1-620 <br/>
A; Residues: 1-620 <br/>
A; Residues: 1-620 <br/>
A; Experimental source: spinal cord
A; Rote: the species of quail is not identified
A; Note: the species of quail is not identified
A; Accession: 803356
A; Residues: 18-31;119-132;135-157;563-569, X', 571 <br/>
A) Accession: S0336
A; Residues: 18-31;119-132;135-157;563-569, X', 571 <br/>
A; Residues: 19-31;119-132;135-157;563-569, X', 571 <br/>
A; Residues: 18-31;119-132;135-157;563-569, X', 571 <br/>
C; Comment: This sprotein is expressed on all external membranes of Schwann cells.
C; Superfamily: myelin-associated glycoprotein; immunoglobulin homology
C; Reywords: glycoprotein; transmembrane protein<br/>
F; 1-17/Domain: signal sequence #status predicted <SIG><br/>
F; 1-17/Domain: immunoglobulin homology cimhs<br/>
F; 31-101/Domain: immunoglobulin homology cimhs<br/>
F; 322,314,331,405,449/Binding site: carbohydrate (Asn) (covalent) #status predicted
Schwann cell myelin protein precursor - Japanese quail C; Species: Coturnix cournix japonica (Japanese quail) C; Date: 17-U11-1992 #sequence_revision 17-Ju1-1992 #text_change 09-Ju1-2004 C; Date: 17-U11-1993 #sequence_revision 17-Ju1-1992 #text_change 09-Ju1-2004 C; Accession: JH0593; PS0356 R; Pulac, C:, Tropak, M.B.; Cameron-Curry, P.; Rossier, J.; Marshak, D.R.; Roder, J.; Le Neuron 8, 32-334, 1992 A; Jille A; Reference number: JH0593; MUID:92153423; PMID:1739462 A; Reference number: JH0593; MUID:92153423; PMID:1739462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 LONRVLSSSHPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRV 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          292 MVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGV 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | : | : | : | : | : | : | | : | | : | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----FGSPYPKNYPPVVARSRPSSAVHESFAGRASFLGDPTGRDCTLNI--ARLSEBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -------MNDGFFLKVTV--LSFTPRPQDHNTDLTCHVDFSRKGVSAQRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VRLRVAYAPRDLVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 RGSEVLREE---PGRNLRLLLSNVGPDDGGSFSCVAENRHGRHNRSLQLRVAYAP---RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPAPSLRWWLGEELLEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   436 IPDSSLVFELPTRNQTVSDGHRDFTAAPPGSDGSITGILTLRGPLEPRLLVLCAARNRHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        471 AQSGSILQLPDKKGLISTAFSNGAFLG-IGITALLFLCLALIIMKILPKRRTQTETPRPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLLSSLLGGSQAMDGRFWIRVQESVMVPBGLCISVPCSFSYPRQDWTGSTPAY--GYWFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 LVLTVLLMGTGCISAPWAAWMPPKWAALSGTCVQLPCRFDYPEE----LRPASIGGLWY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          352 LELPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHYSPKLLGPS-CSWEAEGLHCSCSSQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 AVTETTKGAP-----VATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.6%; Score 392; DB 2; Length 620;
ilarity 23.5%; Pred, No. 4e-18;
Conservative 89; Mismatches 270; Indels 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 -SQYFFRVERGSYVRYNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 169; Conserv
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42;

A,Molecule type: nucleic acid A,Residues: 1-868 4-70R> A,Experimental source: B cell lymphoma 38C13 A,Note: sequence extracted from NCBI backbone (NCBIP:116156)

	136 FLKVT		SOORALDLSVOYPPENLRVMVSOANRTVLENLGNGTSLPVLEGGELCLVCVTHSSPPA 330	SPKLLGPS		VVPTAGPLAOKRNOKATENSPRIPLPPGAPSPESKKNQKKGYQLPSFPEP 591
KAVTETTKGAPVA : DKATKKFKGT-VI RGS	FLKVT ITSVTPSVTSTTSS RVAYAP DVKYTPKLEIKVNP	MSKLILHSVTKDW LLCAADSQPPAT- : :: LICESLASPSATW	SOCRALDLSVQ 	SPKLLGPS APRDVKVLKVSPALHGSCSSQ	SDSGNYNCHANS 3PWANSS	VVPTAGPLAOKRNOKATENS :: NSSGQSFFVRNKKARKSSTQAPESQES :: AGDAGTPATQAPPPNNSDSV EARMPKGTQADYAEVK 637 :: GAKEDVDYVTLK 861
	136 187 175 246	201 306 216 366	273 421 331 466	387 519 402 579		542 739 790 790 850
8 8 8 8	à 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	& a & a	8 6 6 8		3 & & & &	2 2 2 2 2 2

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-----GDTQEKLRIPKVSPWHAGNYSCLAENRLGHGKIDQEAKLD--VHYAP----- 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            441 KAVITVIOSF-----TPILEGDSVILVCRYNSSNPDVTSYRWNPQGSGSVLK-----PG 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLRIQKVTWD-SMPVSCAACNHKCSWALPVILNVHYAPRDVKVLKVSPASEIRAGQRVLL 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----LHCSCSSQASPAPSLRWWL 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----GEELLEGNSSQDSFEVTPSSAGP-----WANSS-LSLHGGLSSG 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               609 QVLYAPRRLRVSIIPGDHVMEGKKATLSCE---SDANPPISQYTWFDSSGQDLH---SSG 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LRLRCEAMNV------HGAQSG-----SILQLPDKKGLISTAFSNGAFLGIGI 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KOGRVTFLGNRI-DNCTLKIHPIRANDSGNLGLRMTAGTERWMEPIHLNVSEKPFQPYIQ 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MPSEIRESQSVTLTCGLNFSCFGYDILLKWFLEDSEITSITSSVTSITSSVTSSIKNVYT 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               276 MTCRVNSSNPKLRTVAVSWFKDGRPLEDQELEQEQQMSKLILHSVTKDMRGKYRCQASND 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---GNVPYLE------AQKGQFLRLLCAADSQPPAT-LSWVLQNRVLS 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                336 IGPGESEEVELTVHYAPEPSRVHIYPSPÅEEGQSVELICESLASPSATNYTWYHNRKPIP 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 SSHPWGPRPLGLELPGVXAGDSGRYTCRAENRLG----SQQRALDLSVQYPPENLRVMVS 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                716 CLTIFI-LAIWGMKIQKKWKQNRSQQGLQE-------NSSGQSFFVRNKKA 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               558 TPNSPRTPLPPGAPSPESK-----KNQKKQYQLPSFPEPKS------STQAPESQE 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---QEELHYATLNFPGVRPRPEARMPKGTQADYAEVK 637
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                                                                                                                                                                                         EGACIRIPCKYKTPLPKARLDNILLPONYEFDKATKKFTGTCLYNATKTEKDPESELYLS 97
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                                                                                                                             33 EGLCISVPCSFS--YPRODWIGSTPAYGYWFKAVIETTKG-----APVAINHQSREVEMS
                                                                  Gaps
                                                              365;
Length 868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --VLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAP-----
                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                             ----FMNDGFFLKVT---
                                                                                                                                                                                                                                                                  TRGREQLIGDPAKGNCSLVIRDAOMODESQYFFRVERGS---
   DB 2;
9.0%; Score 305.5; DB 2;
larity 21.3%; Pred. No. 2.9e-12;
Conservative 92; Mismatches 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -CS------WEAEG------
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Query Match
Best Local Similarity
Matches 192; Conserv
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A65Pedies: Nus musculus (house mouse)
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C.5Spedies: Nus musculus (house mouse)
C.5Spedies: Nus. 15 Law, C.L.; Santons-Argumedo, L.; Kirkham, P.A.; Grabstein, K.; Parkhouse, M. Tamunol. 149, 2641-2649, 1992
A65Pedies: Nus. 149, 2641-2649, 1992
A65Pedies: Musculus homologue of CD22, a B lympho A65Pedies: Mulb:93017867; PMID:1401903
A67Sedies: A46512
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RESULT 10 JH0371 B-cell adhesion protein CD22 beta splice form precursor - human

N;Alternate names: B-cell membrane protein CD22 C;Species: Homo sapiens (man) C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 09-Jul-2004	OY 327 SPPARLSWTQRQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSV 384
	QY 385 HYSPKLLGPSCSWEARGLHCSCSSQASPAPSLRWMLGEELLEGNSSQDSFE- 435
Ajinte: Cubra Cioning of the B cell membrane protein CD22: a mediator of B-5 cell intera Ajieference number: JH0371; MUID:91086838; PMID:1985119 Ajacession: JH0371	502 CIMPROVRVRAINFINSELENSCONGVOLGCUFSS-SHENEVÇETMERAGRILDGANGSTON 436 VIPSSAGPWANSSLSIRLRCEA
T COCC AND THE COCC	
A)CLOSS-TELETERICES: UNITACT: U00928; GB:AD39390; AID:GB:BDN:CAM4Z008.1; FID:GB:BA; A)EXperimental source: B lymphocyte A)Experimental source: B lymphocyte A)Note: the authors translated the codon AAT for residue 358 as Met B.Wilson G T. Waffeld V . Kozlow E . Mennirer J . Ward D . Kehrl J H	OY 466TA 489
the human CD22 gene	490
A;Accession: 156171 A;Status: translated from GB/EMBL/DDBJ	678 YYSPETIGRRVAVGLGSČLAILÍLAÍCGLKLORRWKRTÓSQOGLOENSSGOSFFVRNKKV
A,Molecule type: DNA A,Residues: 121-269,'T',271-473,'K',475-614,'R',616-638,'Y',640-711,777-847 <wil2> A,Cross.references: GB:S61375; NID:g385980; PIDN:AAC18956.1; PID:g3184492</wil2>	Qy 532 RHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESK 576 1 : : : : : : : Db 738 RRAPLSEGPHSLGCYNPMMEDGISYTTLRFPEMNIPRTGDAESSEMQRPPRTCDDTVTYS 797
C;Genetios: A;Gene: GDB:CD22 A;Cross-references: GDB:127545; OMIM:107266	577KNQKKQYQLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQA
A;Map position: 19q13.1-19q13.1 A;Introns: 138/1; 549/1; 359/1; 417/1; 503/1; 591/1; 679/1; 711/2; 804/3 A:Introns: 11400000000000000000000000000000000000	
	841 DYVILK
F/346-396/Domain: immunoglobulin nomology < Inva:> F/609-661/Domain: immunoglobulin homology < INM2> F/688-706/Domain: transmembrane #status predicted <ira> F/6710.112.135.164.231.363.445.448.479.574.664(Rinding site: carbohydrafe (Amn) (coval</ira>	RESULT 11 SSONES
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Query Match 8.6%; Score 289.5; DB 2; Length 847; Best Local Similarity 20.0%; Pred. No. 3.1e-11; Matches 181; Conservative 116; Mismatches 278; Indels 331; Gaps 40;	C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004 C;Accession: S50065 R;Crocker, P.R.; Mucklow, S.; Bouckson, V.; McWilliam, A.; Willis, A.C.; Gordon, S.; Milc
QY 1 MLLPLLISSLIGGSQAMDGRFWI-RVQESVWVPEGLCISVPCSFSYPRQ 48	EMBO J. 13, 4490-4503, 1994 A,Title: Sialoadhesin, a macrophage sialic acid binding receptor for haemopoietic cells v A,Reference number: S50065; MUID:95009950; PMID:7925291 A,Accession: S50065
QY 49 DWTGSTPAYGYWFKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDA 108 :: : : :	A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-1694 <crd> A;Cross-references: UNIPROT:Q62230; EMBL:Z36293; NID:g557253; PIDN:CAAB5290.1; PID:g55725</crd>
OY 109 OMODESCYFFRVERG 123 110 HINDSGQLGLRAMESKTEKWMERIHLNVSERPFPPHIQLPPEIQESQEVTLTCLLNFSCYG 169	Query Match Best Local Similarity 22.0%; Pred. No. 2.2e-10; Matches 135; Conservative 71; Mismatches 199; Indels 209; Gaps 21;
Qy 124 SYVRYNPMNDGFFLKVTVLSFTPRPQDHNTDLTCHV-DFSRKGV 166	QY 5 LLESSLIGGSQAMDGRFWIRÝQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYWFKAV 64
	OY 65 TETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRVERGS 124
191 NTPALE	125 YVRYNFMNDGFFLKVTVLSFTPRP
DD 290 NIFILNENTKLÖGSGKYCCQVSNDVGFGKSEEVFLQVQYAFEFSTVQILHSFAVEGSQV 349 OV 215 RILCAADSOP-PATLSWVLONRVLSSSHPWGPRFIGLELPGVKAGDSGRYTCRAE 268	DD 122 SNKWLDUVKGIIVIVIIDFSFFIIIIFEBELKEGMEKNFNCSIFIICLEGEAGVSDG 1/3 Ov 149
350 EFLCMSLANPLPINYTWYHNGKEMQGRIEBEKUHIPKILPWHAGTYSCVAE	
OY 269 NRIGSOORALDLSVOYPPENLRVMVSQANRTVLENLGNGTSLPVLEGGSLCLVCVTHS 326	Qy 175 RVAYAPRDLVISISRDNTPALEPQPQGNVPYLEAQKGGPLR- 215

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A,Reference number: A40306, MUID:91365376, PMID:1679749
A,Accession: A40306
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A,Molecule type: mRNA
A,Residues: YT, 892-908, R', 910-1101, L',1103-1132, L',1134-1221, L',1223-1397 <KA2>
A)Cross-references: GB:S76436; NID:g243370; PIDN:AAB21121.1; PID:g243371
R; Dodge, G.R.; Kovalazky, I.; Chu, M.L.; Hassell, J.R.; MCBride, O.W.; Yi, H.F.; Iozzo,
Génomics 10, 673-680, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      342 SPSQ------PSDPGV--LELPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHYSP 388
                                                                                                                                                                                                                                          281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   409 VRYPP-----LIPDLTTFLETQAGLVGI-----LHCSVVSEPLATVVLSHGGLTL 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               514 ILINPSAEVVEGQAVTLSCRSGLSPAPDTRFSWYLNGALLLEGSSSSLLLPAASSTDAGS 573
                                                                                                                                                                                                                                                                                                                        354 PQELRYSWYKNHILLEDAH-----ASTLHLPAVTRADIGFYFCEVQNAQGSERSSPLSVV
-LLCAADSQP
                                                                                                              294 FSAAWNDSGAYTCQATNDMGSLVSSPLSLHVFMAEVKMNPAGPVLENETVTLLCSTPKEA
                                                                                                                                                                                                                                    PATL--SWVLQNRVLSSSHPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQORA-LDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     282 VQYPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             454 ASNSGENDFNPRFRISSAPNSLRIEIRDLQPADSGEYTCLAVNSLGNSTSSLDFYANVAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                389 KLIGPSCS-WEAEGLHCSCSSQASPAPSLR--WWL-GBELLEGNSSQ------DS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                574 YYCRTQAGPNTSGP 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           434 F----EVTPSSAGP
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A,Title: Matrix-associated heparan sulfate proteoglycan: core protein-specific monoclonals
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Fi22-4391/Product: perlecan #status predicted <AIG>
Fi22-1391/Pomain: I <DOM1>
Fila4.Fila4.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila6.Fila
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M.; Cassiman, J.J.; van den
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F,4299-4301/Region: motor neuron attachment (L-R-E) motif
F,65,71,76/Findding site: heparan sulfate (Ser) (covalent) #status predicted
F,65,71,76/Findding site: heparan sulfate (Set) (covalent) #status predicted
F,2995,3933,4179/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted
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,Residues: 2166-2171,'X',2173-2175,'X',2177-2185 <HE3>
,Note: peptide potentially matches four different regions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homology
homology
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A;Residues: 1018-1405,'G',1407-1409,'G',1411-1465 <DOD>
A;Cross-references: GB:M64283; NID:g184424; PIDN:AAA22699.1;
R;Heremans, A.; van der Schueven, B.; De Cock, B.; Paulsson,
J. Cell Biol. 109, 3199-3211, 1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;1159-1206/Domain: laminin-type EGF-like homology <LEGS-
;1563-1610/Domain: laminin-type EGF-like homology <BG7>
;1563-1610/Domain: laminin-type EGF-like homology <LEGGS-
;1677-3686/Domain: IV <DOM4>
                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A33625; MUID: 90078352; PMID: 2687294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecule type: protein
Residues: 1379-1384,'X',1386-1388,'X',1390-1398 <HE2>
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repeat |
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F;3888-3921/Domain: EGF homology <EGF>
F;385-4106/Domain: laminin G repeat homology <LG2>
F;4147-4175/Domain: EGF homology <EGF2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F)194-530/Domain: II <DOM2>
F)199-234/Domain: LDL receptor ligand-binding
F)285-319/Domain: LDL receptor ligand-binding
F)325-359/Domain: LDL receptor ligand-binding
F)326-403/Domain: LDL receptor ligand-binding
F)531-1676/Domain: III <DOM3>
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Db 3398 STP Qy 354 LPR Db 3453 LQN Qy 402 LHC Db 3510 Qy 455 -LS Db 3546 ELA	STPTVQVTPQLETKSIGASVEFHCAVPSDGTQLRWFKEGGQLPPGHSVQDGVLR 3452 LPRVQVEHEGEFTCHARHPIGSQHVSLSLSVHYSPKLL	Db 391 TPALRWTKDSTPLGDGPMLSLSSITFDSNGTYVCEASLPTVPVLSRTQNFTLLVQ 445 Qy 386 YSPKLLGPSCSW-EAEGLHCSCSSQASPAPSLRWMLGEELLEGNSSQDSFEVTP 438
RESULT 13 138000 Lutheran blood group glyc Cypecies: Homo saplens (C) patces: Homo saplens (C) Accession: 138000, 8516 Ryarsons, S.F.; Mallinso Proc. Natl. Acad. 851; Mallinso Proc. Natl. Acad. 851; Mallinso A, Title: The Lutheran blo A, Reference number: 13800 A, Molecule type: mRNA A, Residues: 1-628 RES. A, Cross references: UNIPR A, Note: parts of this seq	ESULT 13 Lutheran blood group glycoprotein precursor - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Accession: 138000, S51663 C;Accession: 138000, S51663 C;Accession: 138000, S51663 C;Accession: 138000, G.; Holmes, C.H.; Houlihan, J.M.; Simpson, K.L.; Mawby, W.J. R;Parsons, S.F.; Mallinson, G.; Holmes, C.H.; Houlihan, J.M.; Simpson, K.L.; Mawby, W.J. A;Title: The Lutheran blood group glycoprotein, another member of the immunoglobulin sup A;Accession: 138000 A;Accession: 138000 A;Accession: 188000 A;Accession: 1628 «RES> A;Accession: UNIPROT: P50895; EMBL: X83425; NID: 9603559; PIDN: CAA58449.1; PID: 96035 A;Accession: parts of this sequence, including the amino end of the mature form, were confirm	STR CCRORRENGAPPPGEPGLSHSGSEQPEQ 60 SULT 14 5648 Cell adhesion protein CD22 alpha splice form precu Species: Homo sapiens (man) Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 # Accession: A35648 Title: The B-cell antigen CD22 mediates monocyte a Reference number: A35648; MUID:90231465; PMID:1691 Accession: A35648 Accession: A35648 Accession: A35648
C;Genetics: A;Gene: GDB:LU A;Gene: GDB:LU A;Map position: 19q12-19q13 C;Keywords: glycoprotein F;1-31/Domain: signal seque F;32-628/Product: Lutheram Query Match Best Local Similarity 2 Matches 162; Conservati	netics: Defice: 085-ID9-ID9-ID9-ID9-ID9-ID9-ID9-ID9-ID9-ID9	A,Cross-teferences: GB:X52785, NID:g29778, PIDN:CAA36988.1; PID:g29779 C,Genetics: A,Gene: GDB:CD22 A,Gene: GDB:CD22 A,Gene: GDB:CD22 A,Gene: GDB:CD22 A,Map position: 19q13.1-19q13.1 C,Keywords: alternative splicing; B-cell; cell adhesion; dimer; glycoprotein; transmembre; F;20-510/Domain: signal sequence #status predicted <sig>F;20-510/Domain: extracellular #status predicted <sig>F;20-544/Domain: immunoglobulin homology <imm>F;31-529/Domain: immunoglobulin pemology <imm>F;31-529/Domain: itransmembrane #status predicted <cyt>F;530-647/Domain: intracellular #status predicted <cyt>F;530-647/Domain: intracellular #status predicted <cyt>F;670.112,135,164,231,268,302,397,457/Binding site: carbohydrate (Asn) (covalent) #stē</cyt></cyt></cyt></imm></imm></sig></sig>
17 64 68 116		Query Match 7.3%; Score 245; DB 2; Length 647; Best Local Similarity 21.9%; Pred. No. 1.9e-08; Matches 133; Conservative 72; Mismatches 197; Indels 206; Gaps 26; Qy 1 MLLPLILSSLIGGSQAMDGRFWI-RVQESVMVPEGLCISVPCSFSYPRQ 48
123	YVCVVRAGAAGTAEATARLNVFAKPEATEVSPNKGTLSVMEDSAQEIATCNSRNGNPAPK 182MN-DGFFLKVTVLSFTPRPQDHNTDLTCHVDFS 162	
Qy 163 Db 243 LPB Qy 219 AAI Db 292 RGI Qy 275 Db 347 DVG		Db 110 HLNDSGÖLGLRWESKTEKWMREIHLNVSERPFPPHIQLPPEIQESGEVTLTCLLNFSCYG 169 Qy 124 SYVRYNFWNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVS 167 170 YPIQLQWILLEGVPMRQAAVTSTSLTIKSVFTRSELKFSPQWSHHGKIVTCQLQDADGKFL 229 Qy 168 AQRTVRLRVAYAPRDLVISISRDNTPALEPQPQGNVPY 205 19
Qy 329 PAI	PARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSVH 385	DD 290 LGVLKIONVGMDNTTIACAACNSWCSMASPVALNVQYAPRDVRVRKIKPLSEIHSGNSVS 349

Db 391 TPALRWTKDSTPLGDGFMLSLSSITFDSNGTYVCEASLPTVPVLSRTQNFTLLVQ 445 Qy 386 Y8PKLLGPSCSW-EAEGLHCSCSQASPAPSLRWWLGEELLEGNSSQDSFEVTP 438 446 GSPELKTAEIEPKADGSWREGDEVTLICSARGHPDFKLSWSQLGGSPAEPIP 497 Qy 439 SSAGPWANSSLELHGGLSSGIRRLRCEAWNYHGAGSGSILQLPPKKGLIST 488 Db 498 GRQG-WVSSSLTLKVTSALSRDGISCEASNPHGNKRHVFHFGAVSPQTSQAGVAWAV 554 Qy 489 AFSNGAFLGIGITALLFLCALIMKILPKRRTQTETPRPRFSRHSTILDYINVVPTAGP 548 Db 555 AVSVGLLLILVVAVFYCV	Db 578 CCRQRREKGAP 588 Search completed: November 5, 2004, 13:51:06 Job time: 22.7654 secs							
237LSSSHP		Table 2001 155 #GAM protein - human @ Species: Home sapiens (man) @ Species: Home sapiens (man) #GAM protein - human #GAM protein - 12-Aug-1996 #text_change 09-Jul-2004 #GAM procession: 137202; 847272 #GAM procession: 137202; 8761-5765; 1994 #GAM procession: 137202; 8761-5765; 1994 #GAM procession: 137202; MUD: 95042297; PMID: 7954395 #GAM protein of epithelial cancers: A. Accession: 137202; MUD: 95042297; PMID: 7954395 A. Accession: 137202; MUD: 95042297; PMID: 7954395	e: mRALAY; cranstanced trom Gb/Brbb/DDB0 6: MRSA 588 <resa nces: UNIPROT:P50895; EMBL:X80026; NID:95</resa 	Watch initiarity 23.1%; Prof. No. 3.8 e.08; Matches 155; Conservative 78; Mismatches 223; Indels 215; Gaps 38; Matches 155; Conservative 78; Mismatches 223; Indels 215; Gaps 38; DillesilggsqampgrFWIRVQBSVKVPBGLCISVPCSFSYPRQDWTGSTPAYGY-WFKA 63	64 VTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMODESQ 115	131	QY 219 AADSQP-PATLSWVLONRVLSSSHPWGPRPLGIELPGVKAGDSGRYTCRAENRLGSQ 274	329 PARLSWIQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSVH 385

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November 5, 2004, 13:53:32 ; Search time 109.924 Seconds (without alignments) 2053.348 Million cell updates/sec
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| cgn2 6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
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| cgn2 6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
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| cgn2 6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	Y
Result No.	Score	Query Match	° Query Match Length DB	DB	ID	Description
	3377	100.0		14	US-10-158-238-28	
0	3354	99.3	639	10	US-09-984-130-33	
m	3354	99.3		10	US-09-836-353A-33	Sequence 33, Appl
4	3338	98.8		10	US-09-910-600-28	
ß	3334	98.7		10	US-09-984-130-149	Sequence 149, App
9	3334	98.7		15	US-10-403-938-7	Sequence 7, Appli
7	3334	98.7		16	US-10-614-853-10	Sequence 10, Appl
80	3299	7.76		10	US-09-910-600-9	Sequence 9, Appli
0	2803.5	83.0		10	US-09-910-600-8	Sequence 8, Appli
10	2790.5	82.6	544	σı	US-09-978-295A-259	Sequence 259, App
11	2790.5	82.6		σı	US-09-978-697-259	Sequence 259, App
12	2790.5	82.6		σ	US-09-978-192A-259	Seguence 259, App
13	2790.5	82.6		თ	US-09-999-832A-259	Secuence 259, App

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Sequence 28, Application US/10158238
Publication No. US20030040604A1
GENERAL INFORMATION:
APPLICANT: Immunex Corporation
APPLICANT: Marken, John S.
TITLE OF INVENTION: SIGLEC-12 POLYPEPTIDES, POLYNUCLEOTIDES, AND METHODS OF USE THEREX
CURRENT PILING DATE: 2002-05-29
CURRENT APPLICATION NUMBER: US 60/294,199
PRIOR APPLICATION NUMBER: US 60/294,199
PRIOR FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
SEQ ID NO 28
LENGTH: 639
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US-10-158-238-28
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Best Local Similarity
Matches 639; Conserval
-10-158-238-28
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ORGANISM:
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FKAVTETTKGAPVATNHOSREVEMSTRGRFOLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120
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                                                   ERGSYVRYNFMINDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAP
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Pred. No. 7.5e-220;
0; Mismatches 3;
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Fublication No. US20030129685A1
Fublication No. US20030129685A1
FABERRAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 12 Human Secreted Proteins
FILE REPERBRARS: PF48921
CURRENT APPLICATION NUMBER: US/99/836,353A
CURRENT FILING DATE: 2001-04-18
FRIOR APPLICATION NUMBER: 60/198,407
FRIOR APPLICATION NUMBER: 60/198,407
FRIOR APPLICATION NUMBER: 60/198,407
FRIOR APPLICATION NUMBER: 60/105,971
FRIOR FILING DATE: 1999-10-27
FRIOR FILING DATE: 1999-10-28
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PATENTING DATE: 1988-10-28
NUMBER OF SEQ ID NOS: 147
LENGTH: 639
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Best Local Similarity 99.5%;
Matches 636; Conservative
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Pred. No. 7.5e-220;
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FITLE OF INVENTION: 12 Human Secreted Proteins
FIER REFERENCE: PF48892
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PRIOR PILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 69/836,353
PRIOR APPLICATION NUMBER: 60/198,407
PRIOR PLING DATE: 2000-64-19
PRIOR PLING DATE: 2000-64-19
PRIOR PELING DATE: 1990-10-27
PRIOR APPLICATION NUMBER: PCT/US99/25031
PRIOR PILING DATE: 1990-10-27
PRIOR FILING DATE: 1990-10-28
NUMBER OF SEQ ID NOS: 149
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CURRENT FILING DATE: 2001-10-29
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Publication No. US20030055231A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 99.5%;
Matches 636; Conservative
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SEQ ID NO 33
LENGTH: 639
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ORGANISM: Homo sapiens
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61 FKAVTETTKGAPVATNHQSRBVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV

61 FKAVTETTKGAPVATNHQSREVEMSTRGREQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120

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Pred. No. 1.9e-218;
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US-09-984-130-149
i Sequence 149, Application US/09984130
i Publication No. US2030055231A1
i Publication No. US20330055231A1
i APPLICANT: Ni et al.
i TITLE REPERENCE: PE489P2
CURRENT APPLICATION NUMBER: US/09/984,130
CURRENT PILING DATE: 2001-10-29
i PRIOR PPLICATION NUMBER: 60/243,792
PRIOR FILING DATE: 2000-10-30
i PRIOR FILING DATE: 2000-10-89
i PRIOR FILING DATE: 2000-10-89
i PRIOR FILING DATE: 2000-04-18
i PRIOR FILING DATE: 2000-04-19
i PRIOR FILING DATE: 1999-10-27
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i PRIOR FILING DATE: 1999-10-27
i PRIOR FILING DATE: 1998-10-28
i NUMBER OF SEO ID NOS: 149
i EBNTHH SEOTEMATION NUMBER: 60/105,971
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CORGANISM: Homo sapiens
US-09-984-130-149
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       FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120
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98.8%; Score 3338; DB 10; Length 697;
Best Local Similarity 91.7%; Pred. No. 1e-218;
Matches 639; Conservative 0; Mismatches 0; Indels 58;
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; OTHER INFORMATION: Description of Artificial Sequence: L3-995-2
US-09-910-600-28
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US-09-910-600-28

Sequence 28, Application US/09910600

Publication No. US20030036631A1

GENERAL INPORMATION:
APPLICANT: Longphre, Malinda
APPLICANT: Chang, Han
APPLICANT: Whitney, Gena
TITLE OF INVENTION: NOVEL SIGLECS AND USES THE
FILE REFERENCE: D0003NP
CURRENT APPLICATION NUMBER: US/09/910,600
CURRENT APPLICATION NUMBER: 00/120

PRIOR APPLICATION NUMBER: 60/220,139
PRIOR FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 32

SOFTWARE: PATENTING VET: 2.0

SEQ ID NO 28

LENGTH: 697

TAPPE: TAPE
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ORGANISM: Artificial Sequence
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Matches

TYPE: PRT ORGANISM: Homo sapiens

"", ORGANISM: Ho US-10-403-938-7

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Pred. No. 1.9e-218;
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                                                                                                                                                                                                       ERGSYVRYNFMNDGFFLKVT---
91.5%;
                     Matches 638; Conservative
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SHERMAN FONG
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APPLICANT: HENRY CHIU
 Local Similarity
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Publication No. US20040025195A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: NOVEL HUMAN CELL SURFACE PROTEIN WITH IMMUNOGLOBULIN FOLDS,
TITLE OF INVENTION: BGS-19
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                                     MILIPLILISSILIGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRODWTGSTPAYGYW
                                                                        1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRODWTGSTPAYGYW
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 0; Mismatches
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CURRENT APPLICATION NUMBER: US/10/403,938
CURRENT FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: U.S. 60/368,422
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 88
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638; Conservative
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APPLICANT: WILLIAM WOOD
APPLICANT: WILLIAM WOOD
APPLICANT: THOMAS WU
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE
TITLE OF INVENTION: RELATED DISEASES
FILE REFERENCE: P1973R1-US
                                                                                                                           1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
                                                            1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
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58; Gaps
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CURRENT FILING DATE: 2003-07-08
PRIOR APPLICATION NUMBER: US 60/394,485
PRIOR FILING DATE: 2002-07-08
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SEQ ID NO 10
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                                                                                          Query Match
97.7%; Score 3299; DB 10;
Best Local Similarity 100.0%; Pred. No. 4e-216;
Matches 622; Conservative 0; Mismatches 0;
SOFTWARE: Patentin Ver.
SEQ ID NO 9
LENGTH: 622
                            LENGTH: 622
TYPE: PRT
CRGANISM: Homo sapiens
US-09-910-600-9
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                                                                     Length 697;
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                                                                    Query Match 98.7%; Score 3334; DB 16; Best Local Similarity 91.5%; Pred. No. 1.9e-218; Matches 638; Conservative 0; Mismatches 1;
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; Publication No. US20030036631A1
; GENERAL INFORMATION:
; APPLICANT: Longphre, Malinda
; APPLICANT: Chang, Han
APPLICANT: Chang, Han
; APPLICANT: Whitney, Gena
; TITLE REPERENCE: DO003NP
; CURRENT APPLICATION NUMBER: US/09/910,600
; CURRENT FILING DATE: 2001-07-20
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 32
    ; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-614-853-10
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                 XVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVISISRDNTPALEP
                                                                                  QPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHPWGPRPLGLELPGVKA
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US-09-910-600-8
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                                                                                                                                                                           Score 2803.5; DB 10; Lengthered. No. 1.9e-182; 0; Mismatches 0; Indels
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Patent No. US20020156006A1
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Grimaldi, J. Christopher
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85.1%;
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
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Desnoyers, Luc
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LENGTH: 544
TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: Ashkenazi, Avi
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Best Local Similarity
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US-09-978-295A-259
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241 HPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTV 300 61 FKAVTETTKGAPVATNHQSREVEMSTRGRPQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120 LENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLBLPRVQVE 360 361 HEGEFICHARHPLGSQHVSLSLSVHYSPKLLGPSCSWEAEGLHCSCSSQASPAPSLRWWL 420 GEELLEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQSGSILQLP 480 1 HILLILLESILGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWIGSTPAYGYW RDLVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSS 61 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 121 ERGSYVRYNFWNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAP 1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRODWTGSTPAYGYW Gaps 95; Length 544; Indels DB 9; Score 2790.5; DB 9 Pred. No. 1.5e-181; 0; Mismatches 2; 361 HEGEFTCHARHPLGSOHVSLSLSVHY-REPLICATION NUMBER: 60/084637

REPLICATION NUMBER: 60/084637

REPLICATION NUMBER: 60/084640

REPLICATION NUMBER: 60/084640

REPLICATION NUMBER: 60/084640

REPLICATION NUMBER: 60/084640

REPLICATION NUMBER: 60/084640

REPLICATION NUMBER: 60/084600

REPLICATION NUMBER: 60/084600

REPLICATION NUMBER: 60/084627

REPLICATION NUMBER: 60/084627

REPLICATION NUMBER: 60/084627

REPLICATION NUMBER: 60/086339

REPLICATION NUMBER: 60/086339

REPLICATION NUMBER: 60/08538

REPLICATION NUMBER: 60/08538

REPLICATION NUMBER: 60/08538

REPLICATION NUMBER: 60/085582

REPLICATION NUMBER: 60/085582

REPLICATION NUMBER: 60/085582

REPLICATION NUMBER: 60/085593

REPLICATION NUMBER: 60/085593

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REPLICATION NUMBER: 60/085593

REPLICATION NUMBER: 60/085593

REPLICATION NUMBER: 60/085593 APPLICATION NUMBER: 60/085697 Query Match
Best Local Similarity 84.8%;
Matches 542; Conservative 181 301 PRIOR
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387 -KKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQIETPRPRFSRHSTILDY1 445
                                                                                                                                  446 NVVPTAGPLAQKRNQKATPNSPRTPPPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPES 505
                                                                                         541 NVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPES
481 DKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                601 QESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ 639
                                                                                                                                                                                                                    506 QESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ 544
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CURRENT FILING DATE: 2001-10-16
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Gurney, Austin L.
Hillan, Kenneth J
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Patent No. US20020169284A1
GENERAL INFORMATION:
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APPLICATION NUMBER: 60/064249
FILING DATE: 1997-11-03
APPLICATION NUMBER: 60/065311
FILING DATE: 1997-11-13
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PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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APPLICATION NUMBER: 60/077450
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APPLICATION NUMBER: 60/077641
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Filvaroff, Ellen
Fong, Sherman
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Goddard, Audrey
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APPLICANT: Baker Kevin P.
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APPLICATION NUMBER: 60/080327
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82.6%; Score 2790.5; DB 9; Length 544; 84.8%; Pred. No. 1.5e-181;

Query Match Best Local Similarity

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APPLICATION NUMBER:
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                                                                             APPLICANT: Williams, P. Mickey

***APPLICANT: Wood, William I.

****TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

***ITTLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                    TELLE REFERENCE: P2630PIC9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
FRIOR PAPLICATION NUMBER: 09/918585
FRIOR FILING DATE: 2001-07-30
PRIOR FILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
                                                                                                                                                                                                                                                                                                                FILING DATE: 1997-11-03
APPLICATION NUMBER: 60/065311
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PRIOR APPLICATION NUMBER: 60/066364
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APPLICATION NUMBER: 60/077450
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APPLICATION NUMBER: 60/077649
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PRIOR FILING DATE: 1998-03-20
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PRIOR FILING DATE: 1998-03-26
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APPLICATION NUMBER: 60/079663
FILING DATE: 1998-03-27
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APPLICATION NUMBER: 60/079786
FILING DATE: 1998-03-27
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NG DATE: 1998-03-30
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FILING DATE: 1998-03-30
APPLICATION NUMBER: 60/080105
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APPLICATION NUMBER: 60/080333
FILING DATE: 1998-04-01
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PRIOR FILING DATE: 1998-03-27
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APPLICATION NUMBER: 60/080194
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Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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                                                            umas, Daniel
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APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: PS 5202FC63

FILE REPERENCE: PS 5202FC63

CURRENT APPLICATION NUMBER: U5/09/99,832A

CURRENT FILING DATE: 2001-10-24

PRIOR APPLICATION NUMBER: 06/06250

PRIOR FILING DATE: 1997-11-03

PRIOR FILING DATE: 1997-11-03

PRIOR FILING DATE: 1997-11-13

PRIOR FILING DATE: 1997-11-13

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PRIOR FILING DATE: 1998-03-10

PRIOR FILING DATE: 1998-03-11

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446 NVVPTAGPLAQKRNQKATPNSPRTPPPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPES 505
                                                                                                                        506 QESQEELHYATINFPGVRPRPEARMPKGTQADYAEVKFQ
                                                                  601 QESQEELHYATINFPGVRPRPEARMPKGTQADYAEVKFQ
                                                                                                                                                                                                                                                                Sequence 259, Application US/09999832A Publication No. US20020192706A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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APPLICATION NUMBER: 60/078910
FILING DATE: 1998-03-20
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Pan, James;
Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
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Wood, William I.
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Gerritsen, Mary E
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APPLICANT: Baker Kevin P.
APPLICANT: Botsein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan
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Kuo, Sophia S.
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Jao, Wei-Qiang
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Filvaroff,
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Pred. No. 1.5e-
0; Mismatches
                         PRIOR APPLICATION NUMBER: 60/084598
PRIOR FILING DATE: 1998-05-07
PRIOR PELICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR FILING DATE: 1998-05-07
PRIOR FILING DATE: 1998-05-07
PRIOR PELING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR APPLICATION NUMBER: 60/085339
PRIOR PILING DATE: 1998-05-13
PRIOR PILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
PRIOR PILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
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PRIOR PILING DATE: 1998-05-15
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PRIOR PAPLICATION NUMBER: 60/08559
PRIOR PILING DATE: 1998-05-15
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PRIOR PILING DATE: 1998-05-15
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DR APPLICATION NUMBER: 60/086339
DR FILING DATE: 1998-05-13
DR APPLICATION NUMBER: 60/085338
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Best Local Similarity 94.8
Matches 542; Conservative
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PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
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FAFOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
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FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079920
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FILING DATE: 1998-03-27
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APPLICATION NUMBER: 60/080333
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IG DATE: 1998-04-15
                LICATION NUMBER: 60/079294
ING DATE: 1998-03-25
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FILING DATE: 1998-04-22
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FILING DATE: 1998-03-31
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FILING DATE: 1940
FILING DATE: 1998-03-20
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82.6%; Score 2790.5; DB 9; Length 544; 84.8%; Pred. No. 1.5e-181; iive 0; Mismatches 2; Indels 95; PRIOR PLING DATE: 1998-0-05
PRIOR APPLICATION NUMBER: 60/08414
PRIOR PLING DATE: 1998-05-06
PRIOR PLING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/08441
PRIOR PLING DATE: 1998-05-06
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PRIOR PLING DATE: 1998-05-15 APPLICATION NUMBER: 60/083392 APPLICATION NUMBER: 60/083495 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083496 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083554 FILING DATE: 1998-04-29 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083500 FILING DATE: 1998-04-29 60/083545 LICATION NUMBER: 60/083742 PRIOR FILING DATE: 1998-05-15 PRIOR APPLICATION NUMBER: 60/085697 ICATION NUMBER: 60/083558 APPLICATION NUMBER: 60/083559 CATION NUMBER: 60/085704 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/ FILING DATE: 1998-04-29 938-04-28 FILING DATE: 1998-04-29 FILING DATE: 1998-04-29 1998-04-30 1998-05-Query Match 82.6 Best Local Similarity 84.8 Matches 542; Conservative APPLICATION NUMBER: LING DATE: FILING DATE:

61 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120

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Acids Encoding the Same
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                                                                                                                                                                                                                                      RDLVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSS 240
                                                                                                                                                                                                                                                                                                                                                                          HPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                      241 HPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTV 300
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                                                                                                      ERGSYVRYNFWNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVE 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HEGEFTCHARHPLGSQHVSLSLSVHY-----386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                387 - KKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDVI 445
RDLVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYI
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APPLICANT ASTRONAZI, AVI
APPLICANT BAKER KEWIN P.
APPLICANT BAKER KEWIN P.
APPLICANT BOTSTEIN, DAVI
APPLICANT BOTSTEIN, DAVI
APPLICANT BETON, DAN
APPLICANT FORTARA, NAPOLEON
VPLICANT FILVENEE, Ellen
PPLICANT FORTARA, NAPOLEON
VPLICANT GAO, WEI-CHANG
TLICANT GAO, WEI-CHANG
TLICANT GETTER, MAY E
UCANT GOGOWSKI, PRUI J.
CANT GOGOWSKI, PRUI J.
VANT GUINEY, AUSTIN L.
NATHILIAN, KENNETH J.
NATHILIAN, KENNETH J.
NATHILIAN, ROPER, J.
NATHILIAN, ROPER, J.
NATHILIAN, ROPER, J.
PROMI, SOPPHA S.
FROMI, JAMES,
PROMI, JAMES,
PROMI, JAMES,
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Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Williams, P. Mickey
Wood, William I.
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TITLE OF INVENTION: Acids Encoding the Same PRIDE REPRENCE: PESSOPIC. US/09/978,189
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PRIOR APPLICATION NUMBER: 00/62250
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PRIOR PILING DATE: 13997-10-1730
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Page 14

1998-04-08 NUMBER: 60/081195 1998-04-08 NUMBER: 60/081203 1998-04-09 NUMBER: 60/081255 NUMBER: 60/081955 1998-04-15 NUMBER: 60/081817 1998-04-15 NUMBER: 60/081817 1998-04-15 NUMBER: 60/081817 1998-04-15 NUMBER: 60/081819	NUMBER: 60/08193 1998-04-15 NUMBER: 60/08183 1998-04-15 1998-04-21 NUMBER: 60/08256 1998-04-22 NUMBER: 60/08270 1998-04-22 NUMBER: 60/08270 1998-04-22 NUMBER: 60/08270 1998-04-23 NUMBER: 60/08270 1998-04-23 NUMBER: 60/0833 1998-04-23 NUMBER: 60/0833 1998-04-23 NUMBER: 60/0833 1998-04-28 NUMBER: 60/0833 1998-04-28 NUMBER: 60/08339 1998-04-28 NUMBER: 60/08349 1998-04-28 NUMBER: 60/08349 1998-04-28 NUMBER: 60/08349 1998-04-28 NUMBER: 60/08349 1998-04-28	NUMBER 1999 NUMBER
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APPLICANT: Roy, Margaret Ann
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/978,608A
CURRENT FILING DATE: 2001-10-16
Prior Application removed - See File Wrapper or Palm SEQ ID NO 259
                                                                                                                                                                                                                                                             Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey,
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kujavin, Ivar J.
Kujavin, Ivar J.
Kujavin, Ivar J.
Kujavin, Ivar J.
Kujavin, Ivar J.
Kujavin, Ivar J.
RESULT 15
US-09-978-608A-259
Sequence 259, Application US/09978608A
Publication No. US20030045462A1
GENERAL INFORMATION:
                                                                                                                               APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bottein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan
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CORGANISM: Homo sapiens
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	601 QESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ 639 	506	P 65
505	NVVPTAGPLAQKRNQKATFNSPRTPPPPGAPSPESKKNQKKQYQLPSFPBFKSSTQAPES	446	Д
009	541 NVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPES	541	δ
445	387 -KKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYI	387	Op
540	DKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYI	481	δ
386		387	qq
480	421 GEELLEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQSGSILQLP 480	421	ò
386	二岩	361	qq
420	361 HEGEFTCHARHPLGSQHVSLSLSVHYSPKLLGPSCSWEAEGLHCSCSSQASPAPSLRWWI 420	361	δ

Search completed: November 5, 2004, 14:13:49
Job time : 112.924 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 5, 2004, 13:50:18; Search time 140.458 Seconds (without alignments) 2617.614 Million cell updates/sec

Run on:

US-09-937-636-4 3377 1 MLLPILLSSLLGGSQAMDGR.....RPEARMPKGTQADYAEVKFQ 639 Title: Perfect score: 3 Sequence: 1

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 seqs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ption	Q961c7 homo sapien	OE.	hou	Q96rl6 homo sapien	Bac85493 homo sapi	Q80ze3 mus musculu	Q8by18 mus musculu	O15389 homo sapien	hod	Q920g3 mus musculu	υ	Ĕ	Ĕ	Q96pq1 homo sapien	Ħ	Ø		Aag72479 mus muscu	를	8	SE SE	S S	Q9y286 homo sapien	Q	ŏ	~	043699 homo sapien	ğ	P20916 homo sapien	끍	P20917 mus musculu
OLIMPINA	SILA HUMAN	Q6UXI8	AAQ88703	SILB_HUMAN	BAC85493	Q80ZE3	Q8BY18	SIL5_HUMAN	AAH29896	SILF MOUSE	Q80ZE2	SIL8 HUMAN	072728	SILL_HUMAN	SILL PANTR	Q6PJS0	AAQ79834	AAQ72479	AAH23280	SILS MOUSE	SIL9 HUMAN	Q6GTU4	SIL7 HUMAN	Qeuxgo	AAQ88735	Q8BU57	SIL6 HUMAN	AAH35359	MAG HUMAN	MAG_RAT	MAG_MOUSE
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당	8.7	82.6	2.6	4.3	2.4	3.3	9.4	1.0	8.0	4.8	2.9	1.4	1.3	0.7	0.5	9.5	9.5	9.5	9.	ď	•			18.4	18.4			16.4		14.2	
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## ALIGNMENTS

T 1 SILA HUMAN STANDARD; PRT; 697 AA. S1LA HUMAN STANDARD; PRT; 697 AA. Q56LG7; Q96G54; Q36LC8; 28-FEB-2003 (Rel. 41, Last sequence update) O1-OCT-2004 (Rel. 45, Last annotation update) Sialic acid binding Ig-like lectin 10 precursor (Siglec-10) (Siglec-11) ke protein 2). Name-SIGLEC10; Synonyms-SLG2; Homo sapiens (Human). BixaryCots; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TAXID=9606;	[1] SEQUENCE FROM N.A. (ISOFORMS 1 AND 2). SEQUENCE FROM N.A. (ISOFORMS 1 AND 2). MEDIJINE-21303047; PubMed=11409878; DOI=10.1006/bbrc.2001.5053; Yousef G.M., Ordon M.H., Foussias G., Diamandis E.P.; Wolsecular characterization, tissue expression, and mapping of a novel Siglec-like gene (SLG2) with three splice variants."; Biochem. Biophys. Res. Commun. 284:900-910(2001). [2] SEQUENCE FROM N.A. (ISOFORM 1).	UE=Spleen, INE=21181564; PubMed=11 av J., Kerr S., Ni J., d H., Mattel MG., Moo ntification, characteri a novel human sialic ac hem. J. 355:489-497 (200	SEQUENCE FROM N.A. (ISOPORM 2). TISSUE-Dendritic cell; MEDINE-21359381; PubMed=11358961; DOI=10.1074/jbc.M100467200; MEDINE-21359381; PubMed=11358961; DOI=10.1074/jbc.M100467200; Li N., Zhang W., Wan T., Zhang J., Chen T., Yu., Wang J., Coo X.; Li Oning and characterization of Siglec-10, a novel sialic acid binding member of the Ig superfamily, from human dendritic cells."; J. Biol. Chem. 276:28106-28112(2001).	SEQUENCE FROM N.A. (ISOFORM 3), ALTERNATIVE SPLICING (ISOFORMS 4 AND 5), MUTAGENESIS OF TYR-667, AND INTERACTION WITH PTPN6. MEDIALWESZ15.2896), Pubmed=12163025; DOI=10.1016/\$0006-291X(02)00885-9; Kitzig F., Martinez-Barriocanal A., Lopez-Botet M., Sayos J.; "Cloning of two new splice variants of Siglec-10 and mapping of the interaction between Siglec-10 and SHP-1."; Blochem. Biophys. Res. Commun. 296:355-362(2002).	SEQUENCE OF 337-697 FROM N.A. (ISOFORM 1/3/4). TISSUE=B-cell; MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
17 1 HUMAN SILA HUMAN O961C7; 096 28-FEB-2003 08-FEB-2003 08-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2003 18-FEB-2	SEQUENCE FRC SEQUENCE FRC MEDLINE=213C MI, "Molecular c Siglec-like Biochem. Bic [2]	TISSUE-211E MEDLINE-211E Munday J., F Floyd H., M "Identificat 10, a novel Biochem. J.	SEQUENCE FRC TISSUE=Dendy MEDLINE=2135 Li N., Zhang "Cloning and binding memb	14) 5), MUTAGENN MEDLINE=221E Kitzig F., N "Cloning of interaction Elochem. Bic	SEQUENCE OF TISSUE=B-ce- MEDLINE=2238 Strausberg Klausner R.I Altschul S.I Hopkins R.F
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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Richards S., Worley K.C., Hale S., Garcinaratne P.H.,
Richards S., Worley W.C., Anden A.M., Rodigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA, Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA, Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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RA, Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
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Proc. Natl. Acad. Sci. U.S.A., 99:16899-16003(2002).
Proc. Natl. Acad. Sci. U.S.A., 99:16899-16003(2002).
C.-Innked sialic acid. The sialic acid recognition site may be
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masked by cis interactions with sialic acids on the same cell surface. In the immune response, may act as an inhibitory receptor upon ligand induced tyrosine phosphorylation by recruiting cytoplasmic phosphatase(s) via their SH2 domain(s) that block signal transduction through dephosphorylation of signaling molecules.

SUBUNIT: Interacts with PTPN6/SHP-1 upon phosphorylation.
SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1-4);
secreted (isoform 5).
ALTERNATIVE PRODUCTS:

Event=Alternative splicing, Named isoforms=5; Name=1; Synonyms=Long; IsoId=Q96LC7-1; Sequence=Displayed;

Name=3; Synonyms=Sv3; IsoAeQ96LC7-3; Sequence=VSP_002564; Name=4; Synonyms=Sv4; IsoId=Q96LC7-4; Sequence=VSP_002561; Name=2; Synonyms=Short, Sv1; IsoId=Q96LC7-2; Sequence=VSP_002565;

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EMBL; AY029277; AAK40255.1; -09Y286: 107S EMBL; EMBL; HSSP; EMBL; 

121 ERGSÝVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW 180

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Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chark H.F., Gurney A.L., Crowley C., Currell B., Deuel B., Dowd P., Chan D., Foster J., Grinaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
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Homo.
                                                                                        95;
                                                           DB 2; Length 544;
                                                                                         Indels
PS50815; IG_LIKE; 2.
PS00290; IG_MHC; UNKNOWN 1.
544 AA; 60267 MW; 4DA4E1EFD60AC8CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 HEGEFTCHARHPLGSQHVSLSLSVHY------
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Jamo sapiens (Human).

Enkaryota, Metazoa; Chordata; Craniata; Vertebrata; J

Bammanla; Eutheria; Primata; Catarrhini; Hominidae; J

NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
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                                                          Query Match

82.6%; Score 2790.5; DB 2

Best Local Similarity 84.8%; Pred. No. 4.4e-168;

Matches 542; Conservative 0; Mismatches 2;
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AAQ88703;
02-MAR-2004 (TYEMBLYEL. 27, C.
02-MAR-2004 (TYEMBLYEL. 27, LA
02-MAR-2004 (TYEMBLYEL. 27, LA
SIGLECIO.
    PROSITE; PROSITE; BSEQUENCE
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                                                                                                         WGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLE 302
                                                                                                                                                                                                                                                     GEFTCHARHPLGSQHVSLSLSVHXSPKLLGPSCSWEAEGLHCSCSSQASPAPSLRWWLGE
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                                                                LVISISRDNTPALEPQPGGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: bioinformatics assessment.";
bioinformatics assessment.";
Genome Res. 13:2265-2270(03).

EMBL; AY358337; AAQ88703.1; -..
InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
InterPro; IPR033598; Ig.
InterPro; IPR033508; Ig.
InterPro; IPR033006; Ig.MHC.
Pfam: PF0047; IG; 2.
SMART; SM04409; IG; 3.
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MEDLINE=2288736; PubMed=12975309; Baker K., Baldwin D., Brush J., Clark H.F., Gurney A.L., Abaya E., Baker K., Caldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd E Eaton D., Foster T., Grimaldi C., Gu Q., Hass P.E., Heldens S., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, E
Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
NCBI_TAXID=9606;
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
SIGLEL. 27,
ORFNAMOS=UNQ477;
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Eutheria; Primates; Catarrhini; Hominidae; Homo

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                                                                                                                              "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
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Q96RL6;
28-FEB-2003 (Rel. 41, Created)
01-OCT-2003 (Rel. 45, Last sequence update)
8ialic acid binding Ig-like lectin 11 precursor (Siglec-11) (Sialic Name=SIGLECI1)
Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Sabhagiri S., Simmons L., Singh J., Smith V., Shinson J., Vagta A. Wandlen R., Watenabe C., Wieand D., Woods K., Xie M.H., Yansura X., S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
                                                                                                                                                                                                                                                                                                                            Score 2790.5; DB 2; Length 544; Pred. No. 4.4e-168; 0; Mismatches 2; Indels 95;
                                                                                                                                                                               Bioinformatics Assessment.",
Genome Res. 13:2265-2270(2003).
EMBL; AY358337; AAQ88703.1; -.
SEQUENCE 544 AA; 60267 MW; 4DA4E1EFD60AC8CB CRC64;
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Rest Local Similarity 84.8%;
Matches 542; Conservative
Matches 1 MLLPLLLSSLLGGSQAMD
MLPLLLSSLLGGSQAMD
MLPLLLSSLLGGSQAMD
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Homo sapiens (Human). Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its concent is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003; Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chaw J., Chow B., Chui C., Crowley C., Currell B., Deud B., Chow B., Chui C., Crowley C., Currell B., Deud B., Dewd P., Baton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Lison D., Mark M., Robbie B., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vages A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P., Gray A., The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is referred to
                                                            PTPN11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isold-096RL6-2; Sequence=VSP 008764;
-!- TISSUB SPECIFICITY: Expressed by macrophages in various tissues including Kupffer cells. Also found in brain microglia.
-!- DOMAIN: Contains I copy of a cytoplasmic motif that is referred to as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in modulation of cellular responses. The phosphorylated ITIM motif can bind the SH2 domain of several SH2-
                                                                                                                                    "Cloning and characterization of human Siglec-11. A recently evolved signaling that can interact with SHP-1 and SHP-2 and is expressed by tissue macrophages, including brain microglia."; J. Biol. Chem. 277:24466-24474(202).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- PTM: Phosphorylated on tyrosine residues.
-!- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC (sialic acid binding 1g-like lectin) family.
-!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                        SEQUENCE FROM N.A. (ISOFORM 1), AND INTERACTION WITH PTPN6 AND MEDLINE=22086217; Pubmed=11986327; DOI=10.1074/jbc.M202833200; Angata T., Kerr S.C., Greaves D.R., Varki N.M., Crocker P.R.,

    -!- SUBCELLULAR LOCATION: Type I membrane protein.
    -!- ALTERNATIVE PRODUCTS:

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=Q96RL6-1; Sequence=Displayed;
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InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 3.
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                 NCBI_TaxID=9606;
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FOLTGDPAKGNCSLVIRDAQMQDESQYFFRVERGSYVRYNFMNDGFFLKVTVLSFTPRPQ 149
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                                                                                                                                                                                                                                                                                       02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
CDNA FLJ16033 fis, clone SPLEN2001599, weakly similar to Homo sapiens sialic acid binding immunoglobulin-like lectin 8 long splice variant
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A K
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    ELLEGNSSOGSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCKAWNVHGAQSGSVFQLLPG
                                  KGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINV
                                                                                           543 VPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPESQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 MVPEGLCISVPCSFSYPRODWIGSTPAYGYWFKAVIETIKGAPVAINHQSREVEMSTRGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Spleen,
Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
Pukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
Pukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,
Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
Yamashita H., Mateuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda J.
Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima J.
Wasuho Y., Nagai K., Isogai T.;
"NEDO human cDNA sequencing project.";
Submitted (JUL-2003) to the BMEL/GenBank/DDBJ databases.

EMBL; AK122619; BAC85493.1;
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primata, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 2108.5; DB 2; Length 425;
Pred. No. 4e-125;
1; Mismatches 3; Indels 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 DHNTDLTCHVDFSRKGVSVQRTVRLRVAXAPRDLVISISRDNTPD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             425 AA; 47345 MW; 809854127B397D73 CRC64;
                                                                                                                        590 PSTLGPISQGHQHECSAGSSQDHPPPGA-------
                                                                                                                                                      603 SQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK 637
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421; Conservative
                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                               (Siglec8) gene.
Homo sapiens (F
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Best Local S:
Matches 421
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BAC85493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |||| ||::|::|||||||
122 ERGSRVRHSFLSNAFFLKVTALTKKPDVYIPETLEPGQPVTVICVFNWAFKKCPAPSFSW 181
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GNSSQGSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCKAWN
VHGAQSGSVFQLLPG -> W (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 TGAALSPRTRPSTSHFSVLSFTPSPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPKD
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                                                                                         Extracellular (Potential).

Extracellular (Potential).

Potential.

Cycoplasmic (Potential).

Ig-like V-type.

Ig-like C2-type 1.

Ig-like C2-type 2.

Ig-like C2-type 3.

ITIM motif.

By similarity.

By similarity.

By similarity.

By similarity.

By similarity.

By similarity.

N-linked (GlCNAc. .) (Potential).

N-linked (GlCNAc. .) (Potential).

N-linked (GlCNAc. .) (Potential).

N-linked (GlCNAc. .) (Potential).

N-linked (GlCNAc. .) (Potential).

N-linked (GlCNAc. .) (Potential).

N-linked (GlCNAc. .) (Potential).

N-linked (GlCNAc. .) (Potential).

N-linked (GlCNAc. .) (Potential).

N-linked (GlCNAc. .) (Potential).
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PROSITE; PS50835; IG LIKE; 3.
PROSITE; PS00290; IG_MHC; 1.
Alternative splicing; Cell adhesion; Glycoprotein;
Immunoglobulin domain; Lectin; Phosphorylation; Repeat; Signal;
Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 2173; DB 1; Length 6; Pred. No. 6.2e-129; 50; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /FTIG=VSP 008764.
E -> A (in Ref. 2).
A -> G (in Ref. 2).
FD0EA1936156E5A8 CRC64;
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353
74544 MW;
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                                                                                    84
353
686 AA;
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CONFLICT
SEQUENCE
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CARBOHYD
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182 DAVSFQESRPHTSNYSVLSFIPGLQHHDTELTCQLDFSR--MSTQRTVRLRVAYAPRSLA 239
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STRAIN-C57BL/6J; TISSUE-Thymus;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs.";
Nature 420:563-573 (2002).
                                                                               240 ISIFHDNVSV--PDLHENPSHLEVQQQQSLRLLCTADSQPPATLSWVLEDQVLSWSSPVG
                                                                                                                                                                                        SRTLALELPWYKAGDSGHYTCQAENRLGSQQHTLDLSVLYPPQDLRVTVSQANRTVLBIL
                                                                                                                                                         245 PRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLENL
                                                   185 ISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHPWG
                                                                                                                                                                                                                                                                                                 RNAISLPVLEGQSLCLVCVTYSNPPANVSWAWVTQTLIPIQSSEPGVLELPLVQREHEGE
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
library, clone:A630096C01 product:weakly similar to SIALIC ACID-
BINDING LECTIN (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIKEN FANTOM Consortium; Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-590(2011).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QEELHYATLNFPGVRPRPEARMPKGTQADYAEVK 637
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"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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MEDLINE=99279253; PubMed=10349636;
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STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=21085660; PubMed=11217851;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular analysis of human Siglec-8 orthologs relevant to mouse eosinophils: identification of mouse orthologs of Siglec-5 (mSiglec-F) and Siglec-10 (mSiglec-G)."; Genomics 82:521-530(2003).
                                                                                                                                                                                                                                  510 LIIMKILPKRRTQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPG
                                                                                                                                                                                                                                                                       LLGPSCSWEAEGLHCSCSSQASPAPSLRWWLGEELLEGNSSQDSFEVTPSSAGPWANSSL
                                                                                                                                                                               ------KKGLISTAFSNGAFLGIGITALLFLCLA
                                                                                                                                                                                                                                                                                                                                           APSPESKKNOKKOYOLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGT
                                                                                                                                                                                                                                                                                                                                                                                           356 APSPESKKNOKKOYOLPSFPEPKSSTQAPESQESQESLHYATLNFPGVRPRPEARMPKGT
                                                                                                                            450 SLHGGLSSGLRLRCEAWNVHGAQSGSILQLPDKKGLISTAFSNGAFLGIGITALLFLCLA
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MEDLINE=22921108; PubMed=14559209;
Aizawa H., Zimmermann N., Carrigan P.E., Lee J.J., Rothenberg M.E.,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68;
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InterPro; IPR007110; Ig-11ke.
InterPro; IPR003598; Ig-2.
Ffam; PF00047; Ig; 2.
SMART; SM00408; IG-2.
SMART; SM00408; IG LIKE.
SREQUENCE 688 AA; 76884 MM; 21A619EISOOBFA76 CRC64;
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Last annotation update)
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Best Local Similarity 54.9
Matches 381; Conservative
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Name=Siglec10;
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                                                                      268
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358 RNAISLPVLEGGSLCLVCVTYSNPPANVSWAWVTQTLIPIQSSEPGVLELPLVQREHEGE
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ISIFHDNVSV--PDLHENPSHLEVQQQQSLRLLCTADSQPPATLSWVLEDQVLSWSPVG
                                                                                                                              298 SRTLALELPWVKAGDSGHYTCQAENRLGSQQHTLDLSVLYPPQDLRVTVSQANRTVLEIL
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28-FEB-2003 (Rel. 41, Last sequence update)
01-OCT--2004 (Rel. 45, Last annotation update)
Sialic acid binding Ig-like lectin 5 precursor (Siglec-5) (Obesity-binding protein 2) (OB binding protein 2) (OB-BP2) (CD33 antigen-like
                                                                                                                                                                                               GNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGE
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                                                                                                                                                                                                                                                                                                                                                                   TISSUBE-Erythroleukemia;
MEDLINE-99357812; PubMed=10428856;
MEDLINE-99357812; PubMed=10428856;
Baleaubramanian S., Timans J.C., Peterson D., Bell M.P., Bazan J.F.
Varki A., Kastelein R.A.;
Varki A., Kastelein R.A.;
Immunoglobulin superfamily.";
J. Biol. Chem. 274:22729-22738(1999).
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D., Bell M.P., Bazan J.F.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIŜSUE=Macrophage;
MEDLINE=9840280; PubMed=9731071;
Cornish A.L., Freeman S., Forbes G., Ni J., Zhang M., Cepeda M., Gentz R., Augustus M., Carter K.C., Crocker P.R.;
"Characterization of siglec-5, a novel glycoprotein expressed on myeloid cells related to CD33.";
Blood 92:2123-2132(1998).
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Balasubramanian S., Timans J.C., Peterson
Varki A., Kastelein R.A.;
J. Biol. Chem. 274:28058-28058(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=SIGLEC5; Synonyms=OBBP2, CD33L2;
Homo sapiens (Human)
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                                                             MEDLINE=20499374; PubMed=11042159; Carninci P., Shibata K., Itoh M., Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Muramatsu M., Hayashizaki Y.; Wormalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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C STRAIN-C57BL/GJ TISSUE-Thymus;
C STRAIN-C57BL/GJ TISSUE-Thymus;
A Adachi U., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanamoto K., Hiraoka T., Hirozane T., Haysshida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Horim T., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kolmo H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishinara C., Matsuyama T., Miyazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saito R., Saito H., Sakai K., Shiraki T., Sogabe Y., Tagami M., A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., A Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Hayashizaki Y.; EMBL; AK042488; BAC31272.1; --
ENBL; AK042488; BAC31272.1; --
ENBL; AK042488; BAC31272.1; --
ENBL; AK042488; BAC31272.1; --
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ka T.,
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                                                                                                                                                                                                                                                                                                                STRAIN-CSTBL/64; TISSUE=Thymus;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumnoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watsumiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rikiki integrated sequence analysis (RISA) system-384-format Sequencing pipeline with 384 multicapillary sequencer.";
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Pred. No. 4.4e-97;
3; Mismatches 148; Indels
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GO; GO:0005529; F:sugar binding; IEA.

GO; GO:000157; F:heterophilic cell adhesion; IEA.

InterPro; IPR007110; Ig-like.

InterPro; IPR003599; Ig_C2.
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4.4e-97;
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                                  STRAIN=C57BL/6J; TISSUE=Thymus;
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Caenepeel S., Carrano A.V., Caoile C., Chan Y.M., Christensen M., Cleland C.A., Copeland A., Dalin B., Dehal P., Denys M., Detter J.C., Becobar J., Flowers D., Fotopulos D., Garcia C., Georgescu A.M., Glavina T., Gomez M., Garzales E., Groza M., Hammon N., Hawkins T., Haydu L., Ho I., Huang W., Israni S., Gett J., Kadher K., Kimball H., Kobayashi A., Larionov V., Leem S. H., Lopez F., Lou Y., Lowry S., Martinez D., McCready P.M., Medina C., Morgan J., Nolan M., Ovcharenko I., Pitluck S., Pollard M., Popkie A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J., Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Salth D., A. Slezak T., Solovyev V., Thayer N., Tice H., Tsai M., Ustaszewska A., Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I., Purey T.S., DeJong P., Dickson M., Gordon D., Eichler B.E., Rubin E.M., Lucas S.M., The DNA sequence and biology of human chromosome 19.";

Nature 428:529-535(2004)
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-i- FUNCTION: Putative adhesion molecule that mediates sialic-acid dependent binding to cells. Binds equally to alpha2,3-linked and alpha2,6-linked sialic acid. The sialic acid recognition site may be masked by dis interactions with sialic acids on the same cell surface.

-!- SUBCELULIAR LOCATION: Type I membrane protein.
-!- SUBCELULIAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: Expressed by monocytic/myeloid lineage cells. Found at high levels in professed blood leukocytes, spleen, bone marrow and at lower levels in lymph node, lung, appendix, placenta, pancreas and thymus. Expressed by monocytes and neutrophils but absent from leukemic cell lines representing early stages of myelomonocytic differenciation.
-!- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in modulation of cellular responses. The phosphorylated ITIM motif can bind the SH2 domain of several SH2-

containing phosphatases.
--- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC (stallt acid binding Ig-like lectin) family.
--- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
--- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

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PROSITE; PS50835; IG LIKE; 3.
PROSITE; PS50835; IG LIKE; 1.
Antigen; Cell adhesion; Glycoprotein; Immunoglobulin domain; Lectin; Polymorphism; Repeat; Signal; Transmembrane.
SIGNAL 11 16 Signal; Potential.
CHAIN 17 551 Sialic acid binding Ig-like lectin 5. Potential.
Stalic acid binding Ig-like lectin 5.
Extracellular (Potential).
Cytoplasmic (Potential). Ig-lîke V-type. Ig-like C2-type 1. Ig-like C2-type 2. ITIM motif. SLAM-LIKE MOTIF. By similarity. EMBL; AF170484; AAD50978.1; -. EMBL; U71383; AAB70703.1; -. EMBL; AC018755; AAF87846.1; -. InterPro; IPR007110; Ig-like. InterPro; IPR003598; Ig_c2. InterPro; IPR003006; Ig_MHC. HSSP; Q9Y286; 107S. Genew; HGNC:10874; SIGLECS. Pfam; PF00047; ig; 3. SMART; SM00408; IGC2; 1. MIM; 604200; -DOMAIN TRANSMEM DOMAIN DOMAIN DOMAIN OMAIN AN THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF THE TERMS OF TH

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By similarity.	By similarity.	By similarity.	N-linked (GlcNAc.	N-linked (GlcNAc.	N-linked (GlcNAc.	N-linked (GlcNAc.	N-linked (GlcNAc.	N-linked (GlcNAc.	N-linked (GlcNAc.	N-linked (GlcNAc.	V -> A (in dbSNP:1973019)	/FTIG=VAR 014249.	M -> V (in dbSNP:1807124)	/FTId=VAR 014250.	F -> S (in dbSNP:2278831)	/FTId=VAR_014251.	E -> K (in Ref. 1	R -> W (in Ref. 1	A -> P (in Ref. 1	S -> N (in Ref. 1	MW; 2FEA2B6B341EFEAF CRC64;
101	213	314	100	210	231	253	328	375	384	393	72		215		322		309	358	388	403	60715 MW;
41	164	269	100	210	231	253	328	375	384	393	72		215		322		309	358	388	403	551 AA;
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301 LRRVRSABEGGFTCRAQHPLGFLQIFINLSVYSLPQLIGPSCSWEAEGIHCRCSFRARPA 360
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InterPro; IPR003598; Ig_c2.
Pfam; PF00047; ig; 2.
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Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A stableron M., Soares M.B., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Noriski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

and mouse CDNA sequences.
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                                                                                                   homo sapians (Human).
Eukaryota, Metazoma.
Mammalia, Eutheria, Primata, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.8%; Score 1039; DB 2; Length 551; 39.3%; Pred. No. 2.1e-57; ive 76; Mismatches 204; Indels 114;
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                551 AA; 60688 MW; 6EEA2B6B29B59304 CRC64;
                                        02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Sialic acid binding Ig-like lectin 5.
Homo sapiens (Human).
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                  551 AA
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                PRELIMINARY;
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                                                                                                                                NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                               DEACH. Chem. 276:45128-45136(2001).

PUNCTION: Putative adhesion molecule that mediates sialic-acid dependent binding to cells. Preferentially binds to alpha2,3-linked sialic acid. The sialic acid recognition site may be masked by cis interactions with sialic acids on the same cell surface. SUBCELBULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: Predominantly expressed by immature monocytic/myeloid lineage cells in bone marrow. Also found at lower levels in mature neutrophils and monocytes.

DOMAIN: Contains I copy of a cytoplasmic motif that is referred to as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This
                                                                                                                                                                                                     474 GSILQLPDKKGLISTAFSNGAFLGIGITALLFLÇLALIIMKILPKRRTQTETPRPRFSRH
PSLRWWLGEELLEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQS
                                                                                             361 PSLCWRLEEKPLEGNSSQGSFKVNSSSAGPWANSSLILHGGLSSDLKVSCKAWNIYGSOS
                                                                                                                                                                                                                                                                                                                                                                                                 534 STILDYINVVPTAGPLAQKRNQKATPNSPRTPL-PPGAPSPESKKNQKKQYQLPSFPEPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       motif is involved in modulation of cellular responses. The phosphorylated ITIM motif can bind the SH2 domain of several SH2-
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SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC (siallic acid binding 1g-like lectin) family.
SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mus muscullus (Mouse).
Euksaryota, Bascas, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           092063;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last aunotation update)
01-0CT-2004 (Rel. 45, Last annotation update)
Sialic acid binding Ig-like lectin-F precursor (mSiglec-F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            593 SSTQAPESQESQEELHYATINFPGVRPRPEARMPKGTQA----DYAEVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               479 ED------PIMGTITSGSRKKPWPDSAGDQASPPGDAPP-
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497 SNIALGYPIQGHLNEPGSQTQKEQPPLATVPDTQKDEPELHYASLSFQGPMP-PKPQNTE 555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           407 SSQASPAPSLRWWIGEELLEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRIRCEAW 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecular analysis of human Siglec-8 orthologs relevant to mouse eosinophils: identification of mouse orthologs of Siglec-5 (mSiglec-F) and Siglec-10 (mSiglec-G).", Genomics 8::521-530(2003).

EMBL: AY210401; AA048274.1; -.

HSSP: 09Y286; 107S.

HSSP: 09Y286; 107S.

HSSP: 09Y286; 107S.

InterPro; IPR007110; Ig-like.

InterPro; IPR00715; Ig-like.

InterPro; IPR00715; Ig-2.

SMART; SM00404; Ig-2.

SMART; SM00408; IG-2.

SMART; SM00408; IG-2.

SROSITE, PSS0835; IG-LIKE; 2.

SROSITE, SS0835; IG-LIKE; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=BALB/c;
Display=22821108; PubMed=14559209;
Aizawa H., Zimmermann N., Carrigan P.E., Lee J.J., Rothenberg M.E.
Bochner B.S.;
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 22.9%; Score 772.5; DB 2; Length 523; Best Local Similarity 38.5%; Pred. No. 1.4e-40; Matches 209; Conservative 63; Mismatches 166; Indels 105;
                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                         Q80ZE2;
01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-NAR-2004 (TrEMBLrel. 26,
Siglec-F variant.
                                                                                                                                                                                                      PRELIMINARY;
                                                                                      556 AMKSVÝTĚIK 565
                                           628 GTQADYAEVK 637
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                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                       Name=Siglec5;
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                                                                                   Potential:
Stalic acid binding Ig-like lectin-F.
Extracellular (Potential).
Potential:
Cycoplasmic (Potential).
Ig-like V-type 1.
Ig-like C2-type 1.
ITIM motif.
SLAM-LIKE MOTIF.
           PROSITE: PS5083; IG LIEE; 2.
Cell adhesion; Glycoprotein; Immunoglobulin domain; Lectin; Repeat; Signal; Transmembrane.
CHAIN 17 569 Sialic acid binding Ig-like lectin-F. BOWAIN 17 439 Extracellular (Potential).
DOMAIN 460 60 Potential.
CHAIN 7 460 Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 24.8%; Score 837; DB 1; Length 569; $\frac{2}{2}\text{Best. Local Similarity 35.7%; Pred. No. 1.3e-44;} \text{Matches 239; Conservative 80; Mismatches 207; Indels 144;}
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  SMART; SM00408; IGc2; 1
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569 AA;
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SDNRVQRATILLVSGPK--VSQAGKSETSRGTVLGAIWGAGLMALLAVCLCLIFFTVKVL 465
                                         NVHGAQSGSILQLPDKKGLISTAFSN-----GAFLGIGITALLFLCLALII--MKIL 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isoid=Q9NYZ4-3; Sequence=VSP_002560;
TISSUE SPECIFICITY: Expressed specifically on eosinophils.
DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to
as the immunoreceptor tyrosine-based inhibitor motif (TIIM). This
motif is involved in modulation of cellular responses. The
                                                                                                                                                                                                                                                                                                                                                                                                       cytoplasmic tyrosine-based motifs, and mapping of the siglec8 gene.";
Biochem. Biophys. Res. Commun. 278:775-781(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Eosinophil;
MEDLINE=20092847; PubMed=10625619;
Floyd H., Ni J., Cornish A.L., Zeng Z., Liu D., Carter K.C., Steel J.
"Crocker P.R.;
"Siglec-P.R.; A novel eosinophil-specific member of the immunoglobulin superfamily.";
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 3).

KILLY K.K., Bochmer B.S., Freeman S.D., Tan K.B., Gallagher K.T.,

KILLY K.K., Bochmer B.S., Freeman S.D., Tan K.B., Gallagher K.T.,

D'Alessio K.J., Holmes S.D., Abrahamson J.A., Erickson-Miller C.L.,

Murdock P.R., Tachlmoto H., Schleimer R.P., White J.R.;

Tachrification of SAF-2, a novel siglec expressed on eosinophils,

mast cells, and basophils.",

J. Allergy Clin. Immunol. 105:1093-1100(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 2).

Floyd H., Zhang J.O., Crocker P.R.;

Submitted (OCT 2000) to the EMBL/GenBank/DDBJ databases.

-I. FUNCTION: Putative adhesion molecule that mediates sialic-acid dependent binding to cells. Preferentially binds to adha2,3-linked sialic acid. Also binds to alpha2,6-linked sialic acid. Also binds to alpha2,6-linked sialic acid. Submitted to a site may be masked by cis interactions with sialic acids on the same cell surface.

-I. SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                     Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=20549027; PubMed=11095983; DOI=10.1006/bbrc.2000.3866; Foussias G., Yousef G.M., Diamandis E.P.; "Molecular characterization of a siglec8 variant containing
                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                   (Siglec-8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Stalic acid binding Ig-like lectin 8 precursor
(Sialoadhesin family member-2) (SAF-2)
Name-SIGLEC8, Synonyms-SAF2;
Homo sapiens (Human)
                                                                                                                                                                                   499 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=Q9NYZ4-2; Sequence=VSP_002559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=1; Synonyms=Long;
IsoId=Q9NXZ4-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 3).
                                                                                                                                                                                   STANDARD;
                                                                                          PKR 519
                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                   RKK 468
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PQDPQGQEATDSEYSEIKIHKRETAETQACLRNHNPSSKEV
RG -> VSDVGFSTPSIQPGHL (in isoform 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALTHRPDILILGTLESGHSRNLTCSVPWACKQGTPPMISWI
GASVSSPGPTTARSSVLTLTPKPQDHGTSLTCQVTLPGTGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPLTESWKDGNPLKKPPPAVAPSSGEEGELHYATLSFHKVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MLLLLLLLLLELLWGTKGMEGDRQYGDGYLLQVQELVTVQEGLCVHVPCSFSYPQDGWTDSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MLLPLLLSSLLGGSQAMDG-----RFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGST
phosphorylated ITIM motif can bind the SH2 domain of several SH2-containing phosphatases.
SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC (sialic acid binding Ig-like lectin) family.
SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Static acid binding Ig-like lectin 8.
Extracellular (Potential).
Potential.
Cytoplasmic (Potential).
Ig-like C2-type 1.
Ig-like C2-type 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 721.5; DB 1; Length 499;
; Pred. No. 2.1e-37;
80; Mismatches 152; Indels 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SN00408; TGC2; 1.
PROSITE; PSS0815; IG_LIKE; 2.
Alternative splicing Lold adhesion; Glycoprotein;
Immunoglobulin domain; Lectin; Repeat; Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTSTVRLDVSY -> D (in isoform 2)
/FTId=VSP_002559.
                                                                                                                                                                                                                                                                                                                                EMBL; AF287892; AAG00573.1; -.
EMBL; AF223403; AAF34762.1; -.
EMBL; AF195592; AAF2762.1; -.
EMBL; AF3195092; AAF2762.1; -.
EMBL; AF310531; AAK55140.1; -.
HSSP; Q9Y286; 1078.
Genew; HGNC:10877; SIGLEC8.
MIM, 605639; -.
GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0016488; F:transmembrane receptor activity; TAS.
GO; GO:0001488; F:transmembrane receptor activity; TAS.
GO; GO:0001165; P:signal transduction; TAS.
InterPro; IPR003598; Ig_c2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        086EFF989B74123C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   By similarity.
By similarity.
By similarity.
By similarity.
N'linked (GlorAc...) (N'linked (GlorAc...) (N'linked (GlorAc...) (N'linked (GlorAc...) (N'linked (GlorAc...) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RG -> VSDVGFSTPS:
/FTId=VSP 002560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITIM motif.
SLAM-LIKE MOTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Repeat; S
Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54042 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 30.8 Matches 207; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; ig; 2. SMART; SM00408; IGc2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        416
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CHAIN
DOMAIN
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VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
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61 PVHGYWFRAGDRPYODAPVATNNPDREVQAETQGRFQLLGDIWSNDCSLSIRDARKRDKG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 PAYGYWFKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDES 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212 QFLRILCAADSQPPATLSWVLQNRVLSSSHPWGPRPLGLELPGVKAGDSGRYTCRAENRL 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHYSPKLL 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   392 GPSCSWEAEGLHCSCSSQASPAPSLRWWLGEELLEGNSSQDSFEVTPSSAGPWANSSLSL 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          381 FIIV-----RSCRKKSARPAAGVGDTGMEDAKAIRGSASQGPLTESWKD----GNPLKKP 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPGAPSPESKKNOKKOYOLPSFPEPKSSTQAPESOESQEELHYATLNFPGVRPR-PEARM 625
Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 QYFFRVERGSYVRYNFMNDGFF----LKVTVLSFTPRP-----QDHNTDLTCHVDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 SRK------GVSAQRTVRLRVAYAPRDLVISISRDNTPALEPQPQGNVPYLEAQKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         452 HGGLSSGLRLRCEAWNVHGAQSGSILQLPDKKGLISTAFSNGAFLGIGITALLFL--CLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                510 LIIMKILPKRRIQTETPRPRFSRHSTILDYINVV---PTAGPLAQKRNQKATPNSPRTPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MLLPLLLSSLLGGSQAMDG-----RFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----VTLPG--TGVTTTSTVR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      272 GSQQRALDISVQYPPENIRVMVSQANRTVLENIGNGTSLPVLEGQSLCLVCVTHSSPPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 -----LDVSYPPWNLTMTVFQGDATASTALGNGSSLSVLEGQSLRLVCAVNSNPPAR
                                                                                                                                                                                                                                                                                                                                                                              Length 499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GTSRPVSQVTLAAVG-
                                                                                                                                                                                                                                                                                                                                                                              21.3%; Score 718.5; DB 2; Length 30.8%; Pred. No. 3.3e-37; cive 79; Mismatches 153; Indels
                                                                                                                                  Strausberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO53119; AAH53119.1; -.
InterPro; IPR07110; Ig-like.
InterPro; IPR003598; Ig_c2.
Pfam; PF00047; ig; 2.
                                                                                                                                                                                                                                                                                                                                        54052 MW; CA32FEF7A88A7D3D CRC64;
                     and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                    SMART, SM00408, IGC2; 1.
PROSITE; PSSO835; IG LIKE; 2.
HYDOLHetical protein.
SEQUENCE 499 AA; S4052 MW;
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 30.8%
Matches 207, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   626 PKGTQADYAEVK 637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     346 ----QNEGT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         432 PPAV----
                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                              Hypothetical
SEQUENCE 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
SILL HUMAN
ID SILL HUMAN
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RIAUsner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RIAUsner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Burcow K.H., Schaefer C.F., Bhat N.K.,
Diatchenco, L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Kahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Mrighes R.D., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
M. Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.B.,
    121 SYFFRLERGS-MKWSYKSQLNYXTKQLSVFVTALTHRPDILILGTLESGHSRNLTCSVPW 179
                                                                      162 SRK------GVSAQRTVRLRVAYAPRDLVISISRDNTPALBPQPQGNVPYLBAQKG 211
                                                                                                                                                              212 QFLRLLCAADSQPPATLSWVLQNRVLSSSHPWGPRPLGLELPGVKAGDSGRYTCRAENRL 271
                                                                                                                                                                                                         ----- VTLPG--TGVTTTSTVR---- 240
                                                                                                                                                                                                                                                     272 GSQQRALDLSVQYPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPAR 331
                                                                                                                                                                                                                                                                                           241 ------LDVSYPPWNLTMTVPQGDATASTALGNGSSLSVLEGQSLRLVCAVNSNPPAR 292
                                                                                                                                                                                                                                                                                                                                        332 LSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHYSPKLL 391
                                                                                                                                                                                                                                                                                                                                                                                   293 LSWIRGSLTLCPSRSSNPGLLELPRVHVRDEGEFTCRAQNAQGSQHISLSLS----- 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       452 HGGLSSGLRLRCEAWNVHGAQSGSILQLPDKKGLISTAFSNGAFLGIGITALLFL--CLA 509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----APSSGE-EGELHYATLSFHKVKPQDPQGQ- 463
                                                                                                                   180 ACKQGTPPMISWIGASVS-----SPGP---TTARSSVLTLTPKPQDHGTSLTCO-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----GTSRPVSQVTLAAVG
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
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464 -EATDSEYSEIK 474
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Jones S.J., Marra M.A.;
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NCBI_TaxID=9606;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=22388257; PubMed=124.77932; DOI=10.1073/pnas.242603899;
MEDLINE=22388257; PubMed=12., Schamer C.R., Schaler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Fonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninoi P., Frange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunararne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gabs R.A., Hallyk S.W., Soaresten B.J., Lu X., Gibbs R.A., Halby D.M., Sodergren B.J., Lu X., Gibbs R.A., Halby D.M., Sodergren B.J., Lu X., Gibbs R.A., Now, Mallahy D.M., Green E.D., Dickson M.C., Butterfield Y.S.N., Kzzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Scheintz J., Myers R.M., Generation and Initial analysis of more Han 15,000 full-length human and mouse Cons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Clan J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
Eaton D., Poster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Levis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
"The secreted protein discovery initiative (SPDI), a large-scale
effort to identify novel human secreted and transmembrane proteins: a
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-!- FUNCITON: Putative adhesion molecule that mediates sialic-acid dependent binding to cells. The sialic acid recognition site may be masked by cis interactions with sialic acids on the same cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM LONG).
MEDILINE=21523976; PubMed=11546777; DOI=10.1074/jbc.M105926200;
Angaca T., Varki N.M., Varki A.;
Angaca T., Varki N.M., Varki A.;
"A second uniquely human mutation affecting sialic acid biology.";
J. Biol. Chem. 276:40282-40287(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning and molecular characterization of two splice variants of
new putative member of the Siglec-3-like subgroup of Siglecs.";
Biochem. Biophys. Res. Commun. 284:887-899(2001).
                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
01-0CT-2004 (Rel. 45, Last annotation update)
Sialic acid binding 1g-like lectin-like 1 precursor (Siglec-like molecule 1) (Siglec-LI) (UNQ9215/PRO34042).
Name=SIGLECL1; Synonyms=SLG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Bone marrow, MEDLINE=21303046; PubMed=11409877; DOI=10.1006/Dbrc.2001.5052; Poussias G., Taylor S.M., Yousef G.M., Tropak M.B., Ordon M.H., Diamandis B.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
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Genome Res. 13:2265-2270(2003).
                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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surface.
SUBCELLULAR LOCATION: Type I membrane protein.
ATERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;

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Name=Long; Synonyms=SLG-L;
Isoda=OgFO1-1; Sequence=Displayed;
Name=Short; Synonyms=SLG-E;
Name=Short; Synonyms=SLG-SP 00256;
Isoda=OgFO1-2; Sequence=VSP 00256;
Isoda=OgFO1-2; Sequence=VSP 00256;
Isoda=OgFO1-2; Sequence=VSP 00256;
Isoda=OgFO1-2; Sequence=VSP 00256;
Isoda=OgFO1-2; Sequence=VSP 00256;
Isoda=OgFO1-2; Sequence=VSP 00256;
Interprise small intestine and darenal gland; it is lower expressed in thyroid, beast. The long isoform is highly expressed in spleen, small intestine and bone marrow; it is lower expressed in thyroid, brain and testis.
                                                                                                                                                                                                                                                                             DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to
as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This
motif is involved in modulation of cellular responses. The
phosphorylated ITIM motif can bind the SH2 domain of several SH2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sialic acid binding Ig-like lectin-like
                                                                                                                                                                                                                                                                                                                                                                                 Containing phosphatases.
SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC (similar card binding Ig-like lectin) family.
SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
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Pfam; PF00047; ig; 4.
PR051TE; PS50835; IG_LIKE; 3.
Alternative splicing; Cell adhesion; Glycoprotein;
Immunoglobulin domain; Lectin; Polymorphism; Repeat; Signal;
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Cytoplasmic (Potential)
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EMBL; AF277806; AAK51234.1; --
EMBL; AZ58226; AAK71521.1; --
EMBL; AX358140; AAK35807.1; --
EMBL; BC055809; AAH35809.2; --
HASP; Q97266; 1078.
Genew; HGNC:15482; SIGLECLI.
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127 RYNFMNDGFFLKVTVLSFTPR-----PODHNTDLTCHVDFS-RKGVSAORTVRLRVAY 178
 276:40282-40287(2001)
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nes 198; Conserv
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                                                                                                                                                                    197 IPWDIPVATNTPSGKVQEDTHGRFLLLGDPQTNNCSLSIRDARKGDSGKYYFQVERGSR- 255
                                                                                                                                                                                            RYNFMNDGFFLKVTVLSFTPR-----PQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYA 179
                                                                                                                                                                                                                  256 KWNYIYDKLSVHVTALTHMPTFSIPGTLESGHPRNLTCSVPWACEQGTPPTITWMGASVS 315
                                                                                                                                                                                                                                                                                  240 SHPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRT 299
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                                                                                                                                                                                                                                                                                                                                                                                         418 WWLGEELLEGNSSODSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQSGSIL 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              538 DYINVV---PTAGPLAQKRNQKATPNSPRTPLPP--GAPSPESKKNQKKQYQLPSFPEPK 592
                                                                                                    7 LSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYWFKAVTE 66
                                                                                                                   522 EDANAVRGSASQGPLI----ESPADDSPPHHAPPALATPSPE-----EGEIQYASLSFHK
                                                                                                                                                                                                                                        180 PRDLVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSS
                                                                                                                                                                                                                                                       316 SLD--PTITRSSMLSLIPQPQDHGTSLTCQ------
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BEDLINE-15123976, PubMed=11546777, DOI=10.1074/jbc.M105926200,
Angata T., Varki N.M., Varki A.;
"A second uniquely human mutation affecting sialic acid biology.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pan troglodytės (Chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD; PRT; 597 AA.

0951H0;

28 FFBE-2003 (Rel. 41, Created)

28 FFBE-2003 (Rel. 45, Last sequence update)

01-0CT-2004 (Rel. 45, Last annotation update)

shaltc acid binding Ig-like lectin-like 1 precursor (Siglec-like Name=SIGLECLI).
                                                      Duery Match 20.7%; Score 700.5; DB 1; Length 595; Begt Local Similarity 31.5%; Pred. No. 5.7e-36; Matches 196; Conservative 72; Mismatches 176; Indels 179;
P -> T (in dbSNP:2034891).
/FTId=VAR_014259.
           TIG=VAR 014259.
-> W (in Ref. 3).
D05662176274C5C3 CRC64;
                                                     Score 700.5; DB 1
Pred. No. 5.7e-36;
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                                   64984 MW;
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595 AA;
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                                                                                                                                     -1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- DOMAIN: Contains I copy of a cytoplasmic motif (ITIM). This as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in modulation of cellular responses. The phosphorylated ITIM motif can bind the SH2 domain of several SH2-containing phosphases to the immunoglobulin superfamily. SIGLEC (stails and binding 1g-like lectin) family. SIGLEC (stails can binding 1g-like lectin) family. SIGLEC (SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
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Sialic acid binding Ig-like lectin-like
Mod. Chem. 276:40282-40287(2001).
FUNCTION: Putative adhesion molecule that mediates sialic-acid dependent binding to cells. The sialic acid recognition site may be masked by cis interactions with sialic acids on the same cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR07110; Ig-like.
InterPro; IPR03598; Ig_c2.
Pfan; PF00047; Ig; 4.
SMART; SM00408; IG_c2; 1.
PROSTIE; PS50835; IG_LIKE; 3.
Cell adhesion; Glycoprotein; Immunoglobulin domain; Lectin; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Potential).
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19-13ke V-type 1.
19-13ke V-type 2.
19-13ke C2-type 1.
17-13ke C2-type 2.
17-13ke C2-type 2.
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314	238	345	298	379	358	439	416	476	476	481	536	522	593	561		
KMNYIYDKLSVHVTALTHLPTFSIPGTLESGHPRNLTCSVPWACEQGTPPTITWMGA	APRDLVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLS	SVSSLEPTISRSSMLSLIPKPQDHGTSLTCQ.>>	SSHPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANR	:       :         :	TVLENIGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQ	TASTITIRNGSALSVLEGQSLHLVCAVDSNPPARLSWTWGSLTLSPSQSSNLGVLELPRVH	VEHEGEFTCHARHPLGSQHVSLSLSVHYSPKLLGPSCSWEAEGLHCSCSSQASPAPSL		RWWLGEELLEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQSGSI	Participants	LOLPDKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTI	GAVGGAGATALVFLSFCIIFVVVRSCRKKSARPAVGVGDTG	LDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKS	HILL HILL HILL HILL HILL HILL HILL HILL	STQAPESQESQESLHYATINPPGVRPRPEARMPKGTQADYAEV 636	EGEIQYASLSFHKARPQYPQEQEAIGYEVSEI 593.
258	179	315	239	346	299	380	359	440	417	477	477	482	537	523	594	562
QQ	ò	QQ	δλ	Ор	ò	qq	ò	<b>Q</b> Q	ò	QD	ò	QQ	ò	QQ	δλ	qq

Search completed: November 5, 2004, 13:57:42 Job time : 143.458 secs

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--RNGIALEILQNISYLPVLEGQAIRLLCDAPSNPPAHLSWFQGSPALNATPISNTGILE 300
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 92, Appl Sequence 2, Appl Sequence 2, Appl Sequence 31, Appl Sequence 11, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl		Length 551; Indels 114; Gaps 15;	CSFSYPRODWTGSTPAYGYW 60	SSLVIRDAQMQDESQYFFRV 120 	SSRKGVSAQRTVRLRVAYAP 180	EAQKGOFIRELICAADSOPPATLSWULQNRV 236 :
US-08-389-459A-17 US-08-917-254-95 US-09-517-254-95 US-09-217-254-95 US-09-270-76-43068 US-09-270-76-43068 US-09-261-304-2 S168835-6 S168835-6 SCT US95-08493-13 US-09-823-088A-31 US-09-921-326-14 US-09-991-326-14 US-09-991-326-14 US-09-991-326-14 US-09-707-802-11 US-09-707-802-11 US-09-707-802-11 US-09-707-802-11	ALIGNMENTS 1537A 108/896,537A 19 12,481	Score 1033; DB 4; Pred. No. 4.7e-80; 78; Mismatches 204;	LLPLILSSLI-GGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGS                 : ::  :           :    MLPLILLPLIWGGSLQERPVYELQVQKSVTVQEGLCVLVPCSFSYPWRSWYSS	FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYF  - FRDGELPYYAEVVATNNPDRRVKPETQGRFRLLGDVQKKNCSLSIGDARMEDTGSYF	BEGSYVRYNFMNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYA           : :   :      ERGRDVKYSYQQNKLNLEVTAL	PQGNVPYL
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0	7A-2 , Application of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Seco	30. Similarity 39.				
28 200. 31 199. 33 1 199. 33 2 197. 33 3 193. 34 193. 36 191. 37 198. 44 188. 44 188. 44 188.	RESULT 1 Sequence 2, Applicati Sequence 2, Applicati Patent No. 659008 GENERAL INFORMATION: APPLICANT: Ni, Jian APPLICANT: Gentz, FILE REPERENCE: 1488 CURRENT APPLICATION: FILE REPERENCE: 1488 CURRENT APPLICATION NI FILE REPERENCE: 1488 CURRENT APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI FRICK APPLICATION NI F	Query Match Best Local 8 Matches 253	и н	61	121	181
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COUNTRY:
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                        301 LRRVRSAEKGGFTCRAQHPLGFLQIFLNLSVYSLPQLLGPSCSWEAEGLHCRCSFRAWPA 360
                                                                                                                   361 PSICWRIEEKPLEGNSSQGSFKVNSSSPGPWANSSLILHGGLNSDLKVSCKAWNIYGSQS 420
                                                                                                                                                               474 GSILQLPDKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRH 533
                                                                                                                                                                                         414 PSLRWWLGEELLEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQS 473
                                                                                                                                                                                                                                             534 STILDYINVVPTAGPLAQKRNQKATPNSPRTPL-PPGAPSPESKKNQKKQYQLPSFPEPK 592
354 IPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHYSPKLLGPSCSWEAEGLHCSCSSQASPA
                                                                                                                                                                                                                                                                                     479 ED-----PIMGTITSGSRKKPWPDSPGDQASPPGDAPP-----
                                                                                                                                                                                                                                                                                                                                                    512 -----LEEQKELHYASLSFSEMK----SREPKDQEAPSTTEYSEIK 548
                                                                                                                                                                                                                                                                                                                              593 SSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQA----DYAEVK 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: MUTATIONAL VARIANTS OF MAMMLIAN PROTEINS NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:
APPLICATION UNDER: US/08/759,628
FILING DATE: 05-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49; Mismatches 146;
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41.2%; Pred. No. 5e-
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1: 901 California Avenue
Palo Alto
California
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,574
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 5, Application US/08759628
Patent No. 6225446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Altmann, Scott W.
APPLICANT: Rock, Fernando L.
APPLICANT: Bazan, J. Franado
APPLICANT: Kastelein, Robert A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEG ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acid
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Best Local Similarity 41.23
Matches 186; Conservative
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MEDIUM TYPE: Floppy
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3 LPLLLSSLL-GGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYWF

Indels

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121 RGRDVKYSYQQNKINLEVTALIBKP-------DIHLSGP------ 152
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                                                                                                                  61 RDGBIPYYAEVVATNNPDRRVKPETQGRFRLLGDVQKKNCSLSIGDARMEDTGSYFFRVE 120
                                                                                                                                                                                                                                                                                            182 DLVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQ----PPATLSWVLQNRVL 237
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                                                                                                                                                                      122 RGSYVRYNFMNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPR 181
                                                                                                                                                                                                                                                                                                                                                                                                           238 SSSHPWGPRPLG---LELPGVKAGDSGRYTCRAENRLGSQ---QRALDLSVQYPPENLRV 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 AXSAPWTPRPXAPRELTLTPRPEDHGTNLTCOMK-ROGAOVTTEXTVOLNVSYAPOTITI 243
1 MPLLLLPLLWGGSLQEKPVYELQVQKSVTVQEGLCVLVPCSFSYPWRSWYSSPPLYVYWF 60
                                                       62 KAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          292 MVSQANRIVLENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGV
                                                                                                                                                                                                                                                                                                                                             -----LESGLWRPTRLSCSLPGSCVAGPPLTFSWTGN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: KIKLY, KRISTINE
APPLICANT: ERICKSON-MILLER, CONNIE
TITLE OF INVENTION: Sialoachesin Family Member-2
TITLE OF INVENTION: (SAF-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAPSLCWRLDEKPLEGNSSQGSFKVNSSSAXP 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  412 PAPSLRWWLGEELLEGNSSODSFEVTPSSAGP 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastGEO for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ливя: US/09/038,832
11-MAR-1998
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/041,886
FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09038832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
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REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
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IBM Compatible
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM COR
OPERATING SYSTEM:
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STRANDEDNESS: si
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GENERAL INFORMATION:
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Gaps

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61 PVHGYWFRAGDRPYQDAPVATNNPDREVQAETQGRFQLLGDIWSNDCSLSIRDARKRDKG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212 QFLRLLCAADSQPPATLSWVLQNRVLSSSHPWGPRPLGLELPGVKAGDSGRYTCRAENRL 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          272 GSQQRALDLSVQYPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPAR 331
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                                                                                                                                                                                                                                                                                                               55 PAYGYWFKAVTETTKGAPVATNHOSREVEMSTRGRPQLTGDPAKGNCSLVIRDAQMQDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 QYFFRVERGSYVRYNFMNDGFF----LKVTVLSFTPRP------QDHNTDLTCHVDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 SRK------GVSAQRTVRLRVAYAPRDLVISISRDNTPALEPQPQGNVPYLEAQKG
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                                                                                                                                                                                                                                                                                     1 MLLPLLLSSLLGGSQAMDG-----RFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    332 LSWIQRGOVLSPSQPSDPGVLELPRVQVEHEGEFICHARHPLGSQHVSLSLSV 384
                                                                                                                                                                                                                                             97;
                                                                                                                                                                                                        Length 431;
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Patent No. 6090582
GENERAL INFORMATION:
APPLICANT: KIKLY, KRISTINE
ITILE OF INVENTION:
ITILE OF INVENTION:
CORRESPONDENCE 4
CORRESPONDENCE ADDRESS:
ADDRESSES: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
                                                                                                                                                                                                    Query Match
19.8%; Score 667.5; DB 3;
Best Local Similarity 39.2%; Pred. No. 7.9e-49;
Matches 162; Conservative 52; Mismatches 102;
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COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM:
SOFTWARE: FastESD for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/046,736
FILING DATE: 24-MAR.1998
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 24-MAR-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PPLICATION NUMBER: 60/041,885
FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                  LENGTH: 431 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-038-832-4
TELEX: 846169
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 431 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      272 GSQQRALDLSVQYPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPAR 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 -----LDVSYPPWNLTMTVFQCDATASTALGNGSSLSVLEGQSLRLVCAVNSNPPAR 292
                                                                                                                                                                                                                                                  PAYGYWFKAVTETTKGAPVATNHOSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDES 114
                                                                                                                                                                                                                                                                                       PVHGYWFRAGDRPYQDAPVATNNPDREVQAETQGRFQLLGDIWSNDCSLSIRDARKDKG 120
                                                                                                                                                                                                                                                                                                                                   QYFFRVERGSYVRYNFMNDGFF----LKVTVLSFTPRP------QDHNTDLTCHVDF 161
                                                                                                                                                                                                                                                                                                                                                                                                                     SRK------GVSAQRTVRLRVAYAPRDLVISISRDNTPALEPQPQGNVPYLEAQKG 211
                                                                                                                                                                                               1 MILILILIPLIMGTKGMEGDRQYGDGYLLQVQELVTVQEGLCVHVPCSFSYPQDGWTDSD 60
                                                                                                                                                                1 MLLPLLLSSLLGGSQAMDG-----RFWIRVQESVMVPEGLCISVPCSFSYPRODWTGST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----TGVTTTSTVR----
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    293 LSWTRGSLTLCPSRSSNPGLLELPRVHVRDEGEFTCRAQNAQGSQHISLSLSL 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         332 LSWIQRGQVLSPSQPSDPGVLELPRVQVEHEGEFICHARHPLGSQHVSLSLSV 384
                                                                                                                         Indels 97;
                                                                                   Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09038832
Patent No. 6146845
GENERAL INFORMATION:
APPLICANT: KIKLY, KRISTINE
APPLICANT: ERICKSON-WILLER, CONNIE
TITLE OF INVENTION: (SAF-2)
NUMBER OF SQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAINER & PRESTIA
                                                                                 ; Score 667.5; DB 3;
; Pred. No. 7.9e-49;
52; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
COMPUTER: IBM COMPATIBLE
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 11-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/041,886
FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTATA, PAUL F.
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-50018
TELECOMUNICATION INFORMATION:
TELECHONE: 610-407-0700
TELEFAX: 610-407-0701
                                                                                 Query Match
Best Local Similarity 39.2%;
Matches 162; Conservative 5;
  ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-038-832-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: P.O. BOX 980
CITY: VALLEY FORGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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US-09-038-832-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 YFFRVERGSYVRYNFMNDGFFLKVTVLSFTPRPQDHNT-----DLTCHVDFSRKGVSA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169 GRTVRLRVAYAPRDLVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATL 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229 SWVLQNRVLSSSHPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPEN 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----VTLPGAGV-----TTNRTIQLNVSYPPON 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           289 LRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSD 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243 LTVTVFQGEGTASTALGNSSSLSVLEGGSLRLVCAVDSNPPARLSWTWRSLTLYPSGPSN 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      349 PGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSV--HYSPKLLGPSCSWEAEGLHCSC 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               407 SSQASPAPSLRWWLGEELLEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAW 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          467 NVHGAQSGSILQLPDKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETP 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GAVGGAGATALVFLSFCVIFIVV---RSCRKKSA 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  527 RPRFSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLP 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 LIPLILISSILGGSQAMDGR----FWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 AYGYWFKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQ
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
18.5%; Score 626; DB 3; Length 467;
Best Local Similarity 28.6%; Pred. No. 3.3e-45;
Matches 186; Conservative 79; Mismatches 184; Indels 202; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             587 SPPEPKSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK 637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      303 PLVLEL-QVHLGDEGEFTCRAQNSLGSQHVSLNLSLQQEYTGKM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 PMISWMGISVSPPH--PSTIRSSVLTLIPQPQHHGISLICQ
REGISTRATION NUMBER: 23,031
REFRENCE/DOCKET NUMBER: GH-50019
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
                                                                                                                                                         INPORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
                                                                                                        TELEFAX: 610-407-0701
                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              349 ----SGVLL
                                                                                                                                                                                                                                             TYPE: amino acid STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                       linear
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US-09-046-736-2
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Altmann, Scott W. Rock, Fernando L. Bazan, J. Fernando Kastelein, Robert A.

APPLICANT: APPLICANT: APPLICANT:

APPLICANT:

Sequence 4, Application US/08759628 Patent No. 6225446 GENERAL INFORMATION:

US-08-759-628-4

RESULT 6

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---TVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169 SWMSAAPHLLGPRITQSSVLTITP-AQDHSTNLTCQVTFPGAGVTWERTIQLAVSYAPQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 LVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 WFKAVTETTKGA--PVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 WF-----LEGADVPVATNDPDEEVQEETRGRFHLLWDPRRKNCSLSIRDARRRDNAAYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSF--SYPRQDWTGSTPAYGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MIPLILIPLIMAGALAQERRPOLEGPESLTVQEGLCVLVPCRLPTTLP----ASYYGYGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 317;
OF SEQUENCES: 11
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                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,628
FILING DATE: 05-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.4%; Score 586.5; DB 3; 24.7%; Pred. No. 7.4e-42; cive 73; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05 60/008,574
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REFERRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0552Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 FRVERGSYVRYNFMNDGFFLKV-----
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                                                                                        3: DNAX Research Inst
901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228 VAISIFOGNSAAFK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           440 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 24.78
Matches 172; Conservative
                                                                                                                                                                                                         ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                 California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                     CITY: Palo Alto
STATE: Californ:
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 05 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 ------
                                                                                          ADDRESSEE:
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QY 116 YEFRVERGSYVRYNFWNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLR 175	Db 138 137  Qy 236 VLSSSHPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVVVSQ 295  Db 138	296 ANRIVLENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELP 35  157 GEGTASTALGNSSSLSVLEGQSLRLVCAVDSNPPARLSWTWRSLTLYPSQPSNPLVLEL- 21	OY 356 RVQVEHEGEFTCHARHPLGSOHVSLSLSVHYSPKLLGPSCSWEAEGLHCSCSSQASPA 413	QY 414 PSLRWWLGBELLEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQS 473  Db 256	QY 474 GSILQLPDKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTÇTETPRPRFSRH 533	QY 534 STILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKQYQLPSFPEPKS 593	594 STOAPESQESQEBLHYATLNPPGVRPRPEARMPK 129 HGLAAHSSGEEREIQYAPLSFHKGEPQ-DLSGQE	RESULT 8	US-08-886-537A-3 ; Sequence 3, Application US/08896537A ; Patent No. 6590088 ; GRNERAL, INFORMATION:	; APPLICANT: Ni, Jian ; APPLICANT: Gentz, Reiner L. ; APPLICANT: Rosen, Craig A.	; TITLE OF INVENTION: CL33-LIKE PROFEIN ; FILE REFERENCE: 1488.0480011 ; CURRENT APPLICATION NUMBER: US/08/896,537A ; CURRENT FILING DATE: 1997-07-18 . PRIOR APPLICATION NUMBER: 60/022-481	PRIOR FILING DATE: 1996-07-19; NUMBER OF SEQ ID NOS: 12; SOFTWARE: Patentin version 3.1; SEQ ID NO 3	, TYPE: PRT , ORGANISM: Homo sapiens US-08-896-537A-3	Query Match 13.3%; Score 448.5; DB 4; Length 364; Best Local Similarity 21.4%; Pred. No. 3.9e-30; Matches 149; Conservative 48; Mismatches 110; Indels 389; Gaps 11;	1 MLIPLILSSILGGSQAMDGRFWIRVQESVWVPEGLCISVPCSFSYPRQDWTGSTPAYGYW	Db 1 MPLLLLLPLLWAGALAMDFNFWLQVQESVTVQEGLCVLVPCTFFHPIPYYDKNSFVHGYW 6U Qy 61 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120	Db 61 FREGAIISGDSPVAINKLDOEVQEETQGRFRLLGDFSRNNCSLSIVDARRRDNGSYFFRM 120 Cy 121 ERGSYVRYNFMNDGFFLKVT
423 ELLEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSG 330	ESKKNQKKQYQLPSFPEPKSSTQAPESQE :	Oy 603 SQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK 637 ::	RESULT 7 US-09-046-736-4 ; Sequence 4, Application US/09046736	NNIE	; TITLE OF INVENTION: Staloachesin Family Member-3; NUMBER OF SEQUENCES: 4; CORRESPONDENCE ADDRESS: 7 ADDRESSEB: Rather & Prestia	~ ~ ~	. P. E. B.	M W M	) APPLICATION NUMBER: US/09/046,736 ; FILING DATE: 24-MAR-1998 ; CLASSIRCATION: 514	# PALOR AFPLANTON DAILS: 60/041,885 # APPLICATION NUMBER: 60/041,885 # FILING DAIE: 02-APR-1997 # ATTORNEY/AGENT INFORMATION:	NAME: Prestia, Paul F ; REGISTRATION NUMBER: 23,031 ; REPERBNOS/DOCKET NUMBER: GH-50019 ; TELECOMYNICATION INFORMATION:	TELEFACES: 010-407-0700   TELEFAX: 010-407-0701   TELEX: TELEX:   INFORMATION FOR SEQ ID NO: 4:   SEQUENCE CHARACTERS:	acid scid single inear	; MOLECTLE TYPE: protein US-09-046-736-4 Query Match 15.8%; Score 532.5; DB 3; Length 374;	Best Local Similarity 25.2%; Pred. No. 2.5e-37; Matches 162; Conservative 64; Mismatches 137; Indels 201; Gaps 12;	QY 2 LLPLLLSSLLGGSQAMDGRFWIRVQESVMVPBGLCISVPCSFSYPRQDWTGSTP 55	OY 56 AYGYWFKAVTETTKGAPVATNHOSREVEMSTEGRFOLTGDPAKGNCSLVIRDAQMQDESQ 115 :

121 ERGS-TXYSYRSOLSWHTDLITHERILIPGTLEPGHSRKLLCSVSWACGOGTPPIFSN 141 142	450 Db 116 WEEPSLGV	391 Db 71 YPPKKVIT	48 Qy 77	331 Db 30	; Gaps 13; Qy 24	ty 20.8%; Pred. servative 66; Mis	6.8%; Score	; TYPE: amino acid ; TOPOLOGY: linear ; MOLECULE TYPE: protein US-08-408-095-31	INFORMATION FOR SEQ 1D NO: 31: SEQUENCE CHARACTERISTICS: LENGTH: 501 amino acids	FION INFORMATI (202)293-7060	CLASSIFICATION: 435 ; ATTORNEY/AGENT INFORMATION: ; NAME: Mack, Sugarn J. http://doi.org/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.10	; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/08/408,09 ; FTLING DATE: 21-MAR-1995	disk patible -DOS/MS	ZIF: 20037 COMPUTER READABLE FORM:	603 CITY: Washington STATE: D.C. STATE: D.C. COUNTRY: USA	CORRESPONDENCE ADDRESS: ; ADDRESSE: SUCHRUE, MION, ; CYDERW, 2100 Bondellinesis	TITLE OF INV	483 ; Patent No. 585E ; GENERAL INFORM	255 RESULT 10 US-08-408-095-31 US/08408095 : Secuence 31. Application US/08408095	423	::           :       :         :	363 Qy 620	Db 250 YSPEFRISGAPDKYESEKRIGSERRI	303 Qy 566 LPP	Db 216 ALLIAIVCYITQTRRXKNVTESPSFS	244 QY 506	235 Db 168	179 Db 109
				GSQQRALDLSVQYPPENLRVMVSQANRTVLENL	imitatity 25.1%; FIEG. NO. 4.28-12; ; Conservative 60; Mismatches 146; Indels 77	atch 7.0%; Score 237.5; DB 6; Length	LENGIR: 318 98-5	ATLING DATE: 03-JUN-1987 APPLICATION NUMBER: 516,1 TILING DATE: 21-JUL-1983 NO:::	FILING DATE: 07-FEB-1990 FRICH APPLICATION DATA: APPLICATION NUMBER: 58,620	TIONS, MAINCOS AND DIABNOSTICS USING THE SAME UVERENT APPLICATION DATA: APPLICATION NUMBER: 118/07/476 961	APPLICANT: SUTCLIFFE, J. GERGOR TITLE OF INVENTION: SYNTHETIC POLYBEPTIDES CORRESPONDING PROTEINOID STRANSFARED FROM BRAIN-SPECIFIC MENAS, DREIONS OF PROTEINOID AND DIAMOGRAPHY HERE	T 9 98-5 5 2242798		OEELHYATIMFPGVRPRPBARMPKGTQADYABVKFQ 63	PTAGPLACKRNOKATPNSPRTPLPPGAPSPESKKNOKKOY                  TGSASPKHOKNSK	5	GLISTAFSNGAFLGIGIT	LLEGNSSQDSFEVTPSSA	256	EFTCHARHPLGSQHVSLS	556	LGNGTSLPVLEGQSLCLV	:	PRPLGLELPGVKAGD-SG			LSAAPTSLGPRTTH	121 BRGS-TKYSYKSPQLSVHVTDLTHRPKILIPGTLEPGHSKNLTCSVSWACEQ
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TYCKYNERGES ON PURILY 1194   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   179   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170	121   REGGS - TYPENTEGROUND TO THE TOTAL ENGINE NATION FROM 199   119   119   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120   120	13   EGGS-TWESTERPELAWITDT/HERMILLEP/HERGOLISCHENG/SAGGTPELESS 179   Db   120	13   EGGS - FYGSTREPOLAWIYDD. THEREFULL POLIZEGUESCO TEACH   14   14   14   14   14   14   14   1	13 ERGS-TYRYNSKOLOGY WATURINGERIAL POTTAGES GREATER   199   130   130   131   132   132   132   133   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   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 134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134   134	13   RAGS-TYRYNSKOLOGY   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141  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  141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141	121 BRGS-TKYSYREPOLAWINDLINGHPRILITECTLES-SUSWARCEGOTPPIESM 179   DD   109	121 ERGS-TYCSYKEPOLS/WITTINTREKILIPGTLES-GHSKNIZ-CSVSWACCGOTPPIESW   199   109   109   141   111   111   111   111   111   111   111   112   112   112   112   112   112   112   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113   113  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101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101	121   ERGS-TKYSYKSPOLSVHYTDLTHRPKILIPGTLEBCHSRNLTGSVSWACEGGTPPIFSM 179   Db   109   109   141	121   BRGS-TKYSYKSPOLSVHVTDLTHRPKILIPGTLEDGHSRWLTGSVSRACEGGTPPIFSW   179   Db   109   104   141	121 ERGS-TKYSYKSPOLSVHVTDLTHRPKILIPGTLEPGHSKNLTCSVSWACEGGTPPFISM   179   Db   109   109   141	121	121 ERGS-TKYSYKSPCLSVHVTDLTHRPKILIPGTLEPGHSKNLTCSVSWACEQGTPPIFSW   179   190   109   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141   141  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RDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLS - WVLQNRVLSSSHPWGPR 246
                                                                 PLGLELPGVKAGDSGRYTCRAENRLG-SQQRALDLSVQYPPENLRVMVSQANRTVLENLG 305
                                                                                                                                   306 NGTSLPVLEGQSLCLVCVTHSSPPAR----LSWTQRGQVLSPSQPSDPGVLELPRVQVEH
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                                                                                                                                                                                                                                                                      411 SPAPSLRW--WLGEELLEGNSSQDSFEV-----TPSSAGPWANSSLSLHGGLS----S
                                                                                    210 ---LNFDSISPEDAGSYSCWVNNSIGQTASKAWTLEVLYAPRRLRVSMSPGDQ-----
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                            3: Marshall, O'Toole, Gerstein, Murray & Borun
233 South Wacker Drive, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPATINE: IBM PC Compatible
OPERATINE: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gallatin, W. Michael
APPLICANT: Kilgannon, Patrick D.
TITLE OF INVENTION: ICAM-4 Materials and Methods
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-UJN-1992
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COUNTRY: United States of America
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Patent No. 5700658
GENERAL INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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PRIOR APPLICATION DATA:
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US-08-245-295-2
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383 -CDAALDVDGETLRKNQSSE----LRVLYAPKLDDL-----DCPRSWTWPEGPEQTLH 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49; Mismatches 146; Indels 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2. Application US/08481130
Sequence 2. Application US/08481130
Patent No. 5702917
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Kilgannon, Patrick D.
TITLE OF INVENTION: ICAM-4 Materials and Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESSS:
ADDRESSES: Marshall, O'Toole, Gerstein, Murray & ISTREET: 233 South Wacker Drive, 6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 229; DB 1;
Pred. No. 1.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               441 AGPWANSSLSLHGGLSSGLRLRCEAWNVHGA 471
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FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        United States of America
                                                                                                                                                                                       NAME: BOTUN, MICHAEL F.
REGISTATION UNDRER: 25,447
REPERENCE/DOCKET NUMBER: 2786(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312,474-6300
TELEPAX: 312,474-6448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 917 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.8%;
Best Local Similarity 24.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-245-295-2
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FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: WILLIAMS, JR. JOSEPH A. REGISTRATION NUMBER: 38,659 REFERENCE/DOCKET NUMBER: 27866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 917 amino acids
amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA: APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE
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TELEFAX: 3
                                                                                                                                                         RESULT 13
US-08-656-984A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     431 ------CEARGNPEPS-----VHCARPDGGAVLALGLLGPVTRALAGTYRCT 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267 AENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHS 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     327 SPPARLSWTQRGQVLSPSQPSDPGVLELP-RVQVEHEGEFTCHARHPLGSQHVSLSLSVH 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             519 VPPPSVSCVRSGK-----EBVMEGPLRVAREHAGTYRCEAINARGSAAKNVAVTVE 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         386 YSPKL--LGPSCSW---EAEGLHCSCSSQASPAPSLRWWLGEELLEGNSSQDSFEVTPSS 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 LTGDPAKGNCSLVIRDAQMQDESQYFFRVERGSYVRYNFMNDGFFLKVTVLSFTPRPQDH 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 PEGLCISVPCSFSYPRQDWTGSTPAYGYWFKAVTETTKGAPVATNHQSREVEMSTRGRFQ 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   335 PEGKWYTVSC-----WAGA-----RALV-TLEGIPAAVPGQPAELQLN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ** Query Match 6.8%; Score 229; DB 1; Length 917; ** Best Local Similarity 24.8%; Pred. No. 1.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------VTKNDDKRGFF-
                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,130
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/245,295
FILING DATE: 18-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27866/32713
                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: WILLIAMS, JR. JOSEPH A. REGISTRATION NUMBER: 38,659 REFERENCE/DOCKET NUMBER: 27866 TELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         372 -----
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INPORMATION POR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 917 amino acids
TYPE: amino acid
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APPLICATION NUMBER:
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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510 YGPSFEELGCPSNWTWVEGSGKLFSCEVDGKPEPRVE-CVGS---EGASEGVVLPLVSSN 625
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Best Local Similarity 24.8%; Pred. No. 1.1e-10;
Matches 112; Conservative 49; Mismatches 146; Indels 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: Marshall, O'Toole, Gerstein, Murray & Borun
233 South Wacker Drive, 6300 Sears Tower
                                                                                                                                                                                                                                                              Sequence 2, Application US/08656984A

Patent No. 5753502

GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Kilgannon, Patrick D.
TITLE OF INVENTION: ICAM-4 Materials and Methods
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/656,984A
                                                                                                                       441 AGPWANSSLSLHGGLSSGLRLRCEAWNVHGA 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PATION AUMBER: US 07/827,689
PELING DATE: 27-JAN-1992
PRION APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRION APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRION APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRION APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRION PAPLICATION NUMBER: US 08/102,852
FILING DATE: US 08/25,295
FILING DATE: US 08/25,295
FILING DATE: US MAX-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27866/33321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Chicago
STATE: 111nois
CONTY: United States of America
ZIP: 60605-6402
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
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383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        570 YGPSFEELGCPSNWTWVEGSGKLFSCEVDGKPEPRVE-CVGS---EGASEGVVLPLVSSN 625
                                                                                                                                           152 NTDLICHVDFS--RKGVSAQRIVRLRVAYAPR--DLVISISRDNTPALEPQPQGNVPYLE 207
                                                                                                                                                                             -CDAALDVDGETLRKNQSSE----LRVLYAPRLDDL-----DCPRSWTWPEGPEQTLH 430
                                                                                                                                                                                                                  208 AQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHPWGPRPLGLELPG-VKAGDSGRYTCR 266
                                                                                                                                                                                                                                                  -----CEARGNPEPS------VHCARPDGGAVLALGLLGPVTRALAGTYRCT 471
                                                                                                                                                                                                                                                                                        AENRIGSQQRALDLSVQYPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHS 326
                                                                                                                                                                                                                                                                                                                         AINGOGOAVKDVTLTVEYAP------ALDSVGCPERITWLEGTEASLSCVAHG 518
                                                                                                                                                                                                                                                                                                                                                               SPRARLSWTORGOVLSPSOPSDPGVLELP-RVQVEHEGEFTCHARHPLGSQHVSLSLSVH 385
                                                                      92 LTGDPAKGNCSLVIRDAQMQDESQYFFRVERGSYVRYNFMNDGFFLKVTVLSFTPRPQDH 151
PEGLCISVPCSFSYPRODWTGSTPAYGYWFKAVTETTKGAPVATNHQSREVEMSTRGRFQ 91
                                ---RALV-TLEGIPAAVPGOPAELOLN----
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233 South Wacker Drive, 6300 Sears Tower
                                                                                                         -----VIKNDDKRGFF
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Patent No. 5773293

GENERAL INFORMATION:
APPLICANT: WP, W Michael
APPLICANT: Kilgannon, Patrick D.
TITLE OF INVENTION: ICAM-4 Materials and Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :| ::|:: | | | | : | | | | : | SG--SRNSMI-PGNLSPGIYL-CNATNRHGS 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGPWANSSLSLHGGLSSGLRLRCEAWNVHGA 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-0AN-1992
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/899,724
FILING DATE: 26-MAY-1992
PRICR APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-UN-1992
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-0AN-1993
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floopy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOSTWARE: PatentIn Polating
                                    PEGKMVTVSC-----WAGA--
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STREET: 250
TW: Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.8%; Score 229; DB 1; Length 917; 24.8%; Pred. No. 1.1e-10;
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Patent No. 5852170
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Kilgannon, Patrick D.
TILE OF INVENTION: ICAM-4 Materials and Methods
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
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PILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/245,295
FILING DATE: 16-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, JR. JOSEPH A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32715
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
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amino acid
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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RY: United S
60606-6402
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COUNTRY:
ZIP: 6060
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92 LTGDPAKGNCSLVIRDAQMQDESQYFFRVERGSYVRYNFWNDGFFLKVTVLSFTPRPQDH 151
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24.8%; Pred. No. 1.1e-10;
trive 49; Mismatches 146; Indels 144; Gaps
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               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,595
FILING DATE: PATENTION: 435
PRIOR APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: WILLIAMS, JR. JOSEPH A.
REGISTRATION NUMBERS: 38,659
REFERENCE/DOCKET NUMBER: 27866/32714
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
ERIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
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FILING DATE: 18-MAY-1994
TTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity 24.8%
Watches 112; Conservative
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COMPUTER READABLE FORM:
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## ALIGNMENTS

SAE-4; sialoadhesin family; human; therapy; diagnosis; cancer; inflammation; autoimmune disease; allergy; asthma; inflammation; cerebellar degeneration; Alzheimer's disease; Parkinson's disease; multiple sclerosis, amyotrophic lateral sclerosis; head injury; septic shock; sepsis; stroke; osteoporosis; osteoarthritis; ischemia reperfusion injury; cardiovascular disease; kidney disease; liver disease; myocardial infarction; hypotension; hypertension; AIDS; myelodysplastic syndrome; aplastic anaemia; baldness; infection. Human sialoadhesin family 4 (SAF-1) polypeptide. AAW81023 standard; protein; 639 AA. (first entry) 26-APR-1999 AAW81023; AAW8102 

Homo sapiens 409853840-AL

98WO-US010791. 97US-0047572P. 27-MAY-1998; 27-MAY-1997; 03-DEC-1998.

(SMIK ) SMITHKLINE BEECHAM CORP Kikly KK, Erickson-Miller CL;

WPI; 1999-080779/07. N-PSDB; AAV99911

t 0 - useful New sialoadhesin family 4 polypetides and polynucleotides treat various diseases associated with SAF-4 expression.

Claim 1; Page 31; 48pp; English.

This is the amino acid sequence of new human sialoadhesin family 4 (SAF-4), as deduced from the nucleotide sequence of an isolated cDNA clone (see AAV99911). SAF-4 polynucleotides and polypeptides, and methods for producing such polypeptides in transformed host cells using recombinant techniques are disclosed. SAF-4, its agonists and antagonists, and nucleat acid molecules that enhance or inhibit SAF-4 expression, may be used to treat patients in need of enhancement or inhibition of SAF-4

us-09-937-636-4.nov04.rag

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expression or activity. Conditions that may benefit from such treatment include cancer, inflammation, autoimmunity, allergy, astina, rheumatoid arthritis, CNS inflammation, cerebellar degeneration, Alzheimar, adisease, Parkinson's disease, multiple sclerosis, amyotrophic lateral solerosis, head injury damage and other neurological disorders, septic shock, sepsis, stroke, osteoporosis, osteoarthritis, ischemic injury, cardiovascular disease, kidney disease, liver disease, ischemic injury, wocardial infarction, hypotension, hypertension, ADS, myelodysplastic syndromes and other heamatologic abnormalities, aplastic anaemia, male baldness pattern and bacterial, protozoal, fungal and viral infections related to SAF-4 polypeptide activity. Methods of identifying agonists, anatagonists/inhibitors are also provided, as well as diagnostic assays for detecting diseases associated with inappropriate
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This sequence is a human obesity protein binding protein-2 homologue (hobbensed) of the invention. The hoB-BP2h nucleic acids and polypeptides may be used for the manufacture of a medicament for the treatment of obesity and/or obesity-related disorders. The hoB-BP2h nucleic acids are useful as probes or amplification primers in the detection, quantification or isolation of gene sequences or transcripts, for recombinant expression of hoB-BP2h polypeptides, as immunogens in the preparation and screening of antibodies, and in sense or antisense suppression of one or more hoB-BP2h genes or nucleic acids, host cell or tissue in vivo or in vitro. Antigenic epitope-bearing peptides and oplypeptides are useful for raising of accepting that specifically binds to the hoB-BP2h
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 HPWGPRPLGLELPGVKAGDSGRYTCRAENKLGSQQRALDLSVQYPPENLRVMVSQANRTV
                                               Human obesity protein binding protein-2 homologue, hOB-BP2h, obesity;
obesity-related disorder, therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
                                                                                                                                                                                                                                                                                                                                                                                                                     New human obesity protein binding protein-2 homologue nucleic acids, polynucleotides and polypeptides useful for producing medicament for treating obesity and/or obesity-related disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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             Human obesity protein binding protein-2 homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 3377; DB 3;
100.0%; Pred. No. 2.3e-232;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 9; Page 89-91; 92pp; English
                                                                                                                                                                                                                   22-MAR-2000; 2000WO-US006682
                                                                                                                                                                                                                                                        99US-0127667P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 639, Conservative
                                                                                                                                                                                                                                                                                            (ELIL ) LILLY & CO
                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAA37848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 639 AA;
                                                                                                                                           WO200059942-A2
                                                                                                                                                                                                                                                                                                                                 Wei J;
                                                                                                                                                                                                                                                        02-APR-1999;
                                                                                                           Homo sapiens
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HEGEFTCHARHPLGSQHVSLSLSVHYSPKLLGPSCSWEAEGLHCSCSSQASPAPSLRWWL 420

LENLGNGTSLPVLEGGSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVE

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AAY97543 standard; protein;

RESULT 2 AAY97543

(first entry)

12-FEB-2001

AAY97543;

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The present invention relates to 12 secreted human proteins and the nucleotide sequences encoding them. The polynucleotide sequences given in AAA80606-A80653 encode the 12 secreted protein sequences given in AAB505676-B25593. The human secreted proteins have various activities dependent on the tissues in which they are expressed. Examples of the activities of the proteins include: immunosuppressant; anti-inflammatory; antiarthritic; antirhumatic, dermanological; antiproliferative; antiarteriosclerotic; anticancer; vulnerary; antivixal; antibacterial; and antifungal activity. The proteins, polypeptides, agonists and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acid molecules encoding human secreted proteins are used for the prevention, amelioration and treatment of autoimmune, inflammatory, hyperproliferative and cardiovascular disorders, cancer, wounds, and infectious diseases.
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HEGEFTCHARHPLGSQHVSLSLSVHYSPKLLGPSCSWEAEGLHCSCSSQASPAPSLRWID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein; immunosuppressant; anti-inflammatory; antiarthritic;
                                                   GEELLEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQSGS1LQLP
                                                                                  GEELLEGNSSÕDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQSGSILQLP
                                                                                                                     DKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYI
                                                                                                                                                  DKKGLISTAFSNGAFLGIGITALLFLCLALIMKILPKRRTQTETPRPRFSRHSTILDYI
                                                                                                                                                                                      NVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPES
                                                                                                                                                                                                                      NVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSPPEPKSSTQAPES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kenny JJ, Moore PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CD33-like protein encoded by human secreted protein gene #5.
                                                                                                                                                                                                                                                                                        639
                                                                                                                                                                                                                                                        QESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ 639
                                                                                                                                                                                                                                                                             melanoma; lymphoma; wound healing; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 13A-C; 803pp; English.
                                                                                                                                                                                                                                                                                                                                                                            AAB25580 standard; protein; 639 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN
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antagonists may be used to treat prevent and/or diagnose various disease, disorders and conditions examples of which include: immune disorders e.g. Addison's disease, rheumatoid arthritis, dermatitis, and multiple sclerosis; inflammatory disorders e.g. inflammatory bowel disease, Crohn's disease and nephritis; hyperproliferative disorders such as paraptroleniamemias and purpura; cardiovascular disorders e.g. coronary arteriosclerosis and myocarditis, cancer e.g. melanoma and lymphoma. The proteins and polymucleotide sequences may also be used in wound healing and the treatment of infectious diseases. The human secreted protein gene #5 and protein sequences are represented in sequences AAA80610 and AAB25580. Sequences AAA80649 represent genes related to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                480
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                                                                                                                                                                                                                                                                                                                     1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
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                                                                                                                                                                                                                                                     Score 3354; DB 3;
Pred. No. 1e-230;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                         636; Conservative
                                                                                                                                                                                       secreted protein gene#5
                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                         Sequence 639 AA;
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hemostatic, gene therapy, cancer, inflammation, immune disorder, neurological disorder, blood clotting disorder, food additive, preservative, human, secreted protein.
cytostatic; antiinflammatory; immunomodulator; neuroprotective;
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US2003055231-A1

20-MAR-2003

27-OCT-1999; 99WO-US025031. 19-APR-2000; 2000US-0198407P. 30-OCT-2000; 2000US-0243792P. 18-APR-2001; 2001US-00836353. 2001US-00984130. 29-OCT-2001; 28-OCT-1998;

VI J.
YOUNG P E.
KENNY J J.
OLSEN H S.
MOORE P A. LIU D. CROCKER P R GREENE J M. RUBEN S M. (NIJJ/) (YOUN/) (KENN/) I (GREE/) (RUBE/) (LIUD/) (CROC/) (OLSE/) (MOOR/) (MEIY/)

Greene JM; ۲. Wei Moore PA, Kenny JJ, Olsen HS, Crocker PR; Young PE, M, Liu D, Ruben SM,

WPI; 2003-567103/53. N-PSDB; ADA27034.

New human secreted nucleic acid molecules and polypeptides, useful for preventing, treating, or ameliorating a medical condition, such as cancer, inflammation, immune disorders, neurological and blood clotting disorders.

Claim 11; Fig 13; 454pp; English.

The invention relates to an isolated mucleic molecule that is at least 55% identical to 18 human cDNA sequences representing 12 novel genes CC go encoding secreted proteins or a polymucleotide fragment of the cDNA sequence contained in American Type Culture Collection (ATCC) deposit No. defined in the specification, its species homologue, a variant or allelic sequence contained in American Type Culture Collection for allelic contained in the polymucleotide having a polymucleotide where the polymucleotide having a polymucleotide where the polymucleotide for the polymolations to a nucleic acid molecule comprising a nucleotide sequence of only A or T residues. Also included are recombinant vectors, host cells (for producing the polympetide), the secreted polymeptide (comprising a sequence that is at least 55% identical to a polympetide (comprising a sequence that is at least 55% identical to a polympetide fragment, domain, epitope, full-inaith to protein, variant, allelic variant or species homologue), antibodies that specifically bind to the polympetides, diagnosing, treating, preventing or ameliorating a medical condition by administering the polymucleotide cortivity or a condition protein condition, and detecting an activity in a biological assay (by expressing the cDNA sequence and identifying the protein in the supermatant or a biological assay and identifying the protein or a susceptibility to a condition, such as cancer, inflammation and other immune condition, such as cancer, inflammation and other immune condition, such as cancer, inflammation and other immune condition, such as cancer, inflammation and other immune condition, such as cancer, inflammation and other immune condition, such as cancer, inflammation and other immune condition, such as cancer, inflammation and other immune condition, such as cancer, inflammation and other immune condition, such as cancer, inflammation are also useful for chemistry assays. The polympetides are also useful for central protein and antibodies are useful for trestri 

US2003129685-A1.

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agonist or antagonist may also be used as a food additive or preservative to increase or decrease storage capabilities, fat content or other nutritional components. The present is a secreted protein of the
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The invention relates to an isolated SIGLEC (sialic acid-binding Igrelated lectin) protein (I). Pharmaceutical compositions comprising (I) are useful for treating immune system diseases such as asthma, leukaemia or other allergic or inflammatory diseases. Extracellular domains of (I) represent potential markers for screening, diagnosis, prognosis, follow up assays, and imaging methods. (I) is useful as a target for drugs which inflammation, tissue damage and remodeling in asthma, and inflammation, tissue damage and remodeling in asthma, and inflammation to salege such as allergic rhinitis, osteoarthritis, crohn's disease, psoriasis, rheumatoid arthritis, conjunctivitis, etc. (I) is also useful for monitoring the course of disease or disorders, and for identifying agents that bind with and/or modulate the biological activity of SIGLEC-BMS proteins. The nucleic acid molecules (II) encoding (I) are useful in diagnosis and/or prognosis methods, and to detect the presence and/or amount of SIGLEC-BMS nucleotis methods, and to detect the presence are useful for screening genomic library to isolate a genomic clone of signases or disorders associated with SIGLEC-BMS transcripts or proteins. The SIGLEC-BMS antibodies are also used to detect, sort or isolate cells
11 GEELLEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQSGSILQLP 480
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                                        DKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYI
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N-PSDB; ABK43373.
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Pred. No. 1e-230;
0; Mismatches 3;
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                                                                              28-OCT-1998; 98US-0105971P.
27-OCT-1999; 99WO-US025031.
19-APR-2000; 2000US-0198407P.
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Best Local Similarity 99.5
Matches 636; Conservative
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YOUNG P E.
KENNY J J.
OLSEN H S.
MOORE P A.
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N-PSDB; ADE86564.
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27-OCT-1999;
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181 TGAALSSQGTKPTTSHFSVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAFRD 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          481 ELLEGNSSQDSFEVTPSSAGPWANSESLHGGLSSGLRLRCEAWNVHGAQSGSILQLPDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 WGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 NLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELLEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQSGSILQLPDK
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                                                                                                                                                                                                    1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
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                   expressing SIGLEC-BMS proteins and in diagnostic imaging technology. AAU87074-AAU87089 represent human SIGLEC amino acid sequences of the
                                                                                                                                                               Indels 58; Gaps
                                                                                                                           Length 697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  661 SQEELHYATINFPGVRPRPEARMPKGTQADYAEVKFQ 697
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                                                                                                                             Score 3338; DB 5;
Pred. No. 1.6e-229;
                                                                                                                                                               0; Mismatches
                                                                                                                           98.8%;
91.7%;
AAUb.

Sequence 697 Ax.

Sequence 697 Ax.

Chest Local Similarity 91.7%.

Tiches 639; Conservative

I MLLPLLISSLIGGSON

I HILLISSLIGGS

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ADA27153 standard; protein; 697 AA

ADA27153 RESULT

(first entry)

20-NOV-2003

ADA27153;

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The invention relates to an isolated mucleic molecule that is at least CC 95% identical to 18 human cDNA sequences representing 12 novel genes concoding secreted proteins or a polyvucteotide fragment of the cDNA.

C defined in the specification, its species homologue, a variant or allelic variant of the polymucleotide having a polymucleotide capable of the polymucleotide having a polymucleotide capable of the polymucleotide having a polymucleotide capable of the polymucleotide sequence of only A or T residues. Also included are cereted polypeptide sequence of only A or T residues, 15% included are recombinant vectors, host cells (for producing the polypeptide), the crecombinant vectors, host cells (for producing the polypeptide) the protein, variant, allelic variant or species homologue), antibodies that serviced protein, variant, allelic variant or species homologue), antibodies that specifically bind to the polypeptides, diagnosing, treating, preventing or ampliorating a medical condition by administering the polymucleotide contribution by administering the polymucleotide is equence in a cell, isolating the supernatant, and detecting an activity or in a biological condition, for preventing, treating, or amplibodies are useful for diagnosing a pathological condition or a susceptibility to a pathological condition, such as cancer, inflammation and other immune disorders, neurological and bloopical condition or a susceptibility to a pathological condition, for preventing, treating, or amplicating a condition, such as cancer, inflammation and other immune condition, such as cancer, inflammation and other immune condition, such as cancer, inflammation and other immune condition, such as cancer, inflammation and other immune condition, such as cancer, inflammation or association of the providing immunological probes for differential identification of chromosome identification, radiation which mapping or long-range conditions are negletically probes for differential identification of chromosome identification, radia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human secreted nucleic acid molecules and polypeptides, useful for preventing, treating, or ameliorating a medical condition, such as cancer, inflammation, immune disorders, neurological and blood clotting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wei Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Olsen HS, Moore PA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kenny JJ, O.
Crocker PR;
                                                                                                                                                                                                        2000US-0198407P.
2000US-0243792P.
2001US-00836353.
                                                                                                                                 29-OCT-2001; 2001US-00984130
                                                                                                                                                                                          99WO-US025031
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RUBEN S M.
LIU D.
CROCKER P R.
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YOUNG P E.
KENNY J J.
OLSEN H S.
MOORE P A.
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M, Liu D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ADA27152
                                                       US2003055231-A1.
                                                                                                                                                                                                                                                                                                                                                                                     WEI Y.
                  Homo sapiens
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27-OCT-1999;
                                                                                                                                                                                                             19-APR-2000;
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Greene JM;

Sequence 697 AA;

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                                                                                                                          FKAVTETTKGAPVATNHOSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
                                                                                                                                                                                                                                                                                                                                             241 LVISISRDNIPALEPQPQGNVPYLEAQKGQFLKLLCAADSQPPATLSWVLQNRVLSSSHP
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                                                             MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
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                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human; cell surface protein; immunoglobulin; BGS-19; cytostatic; gynaecological; immunosuppressive; antiinflammatory; antiasthmatic; antidiabetic; dermatological; gene therapy.
                                 58;
    Length 697;
Score 3334; DB 6; Length 69
Pred. No. 3e-229;
0; Mismatches 1; Indels
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                                                                                                                                                                                       ERGSYVRYNFMNDGFFLKVT-------
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 98.78;
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                               638; Conservative
                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                              243
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 Query Match
Best Local (
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542

242

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Homo sapiens
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WO2003083078-A2

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The present invention describes human cell surface protein with changed designated 856-19 (i). (i) has cytocatatic, dynacological, immunosuppressive, antiinflammatory, antiasthmatic, antidiabetic and darmatological activities, and can be used in gene therapy. (I) can be used for preventing treating or ameliorating and can be used for preventing treating or ameliorating and can be used for preventing treating or ameliorating and can be used in garder related to aberrant immunoglobulin receptor activity, adsorder; a disorder call turface receptor activity; a callular adhesion disorder; a disorder callular and treating or ameliorating and sorder callular and treating and adsorder; and ovarian disorder; and sorder callular and treating and and adsorder; and ovarian disorder; ovarian cancer; dysfunction; infertility; pelyic inflammatory disease; candometriosis; placental aromatase deficiency; because for placental dysfunction; infertility; pelyic inflammatory disease; candometriosis; placental characteristics; aberrant showing of female primary sexual characteristics; aberrant showing of conference addressed conference puberty; precocious puberty; precocious puberty; precocious puberty; precocious precocious precocious; premature thelarche; premature puberty; precocious puberty; precocious aberrant ovarian cycle; memorrhagia; merorrhagia; menometorrhagia; menometorrhagia; merorrhagia; menometorrhagia; menometorrhagia; menometorrhagia; menometorrhagia; merorrhagia; menometorrhagia; menometorrhagia; menometorrhagia; menometorrhagia; menometorrhagia; menometorrhagia; menometorrhagia; menometorrhagia; menometorrhagia; menometorrhagia; menometorrhagia; menometorrhagia; menometorrhagia; menometorrhagia; menometorrhagia; menometorrhagia; menometorrhagia; menometorrhagia; menometorrhagia; menometorrhagia; menometorrhagia; menometorrhagia; menometorrhagia; menometorrhagia; menometorrhagia; menometorrhagia; menometorrhagia; menometorrhagia; menometorrhagia; menometorrhagia; menometorrhagia; menometorrhagia; pesitatatic-ovaria
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                                                                                                                                                                                                                                                  New isolated nucleic acid molecule encoding BGS-19 polypeptides, useful for preventing, treating or ameliorating a medical condition, such as a disorder related to aberrant immunoglobulin cell surface receptor
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                                                                                                                                                                     Chen J;
                                                                                                                                                                     Wu S,
                                                                                                                                                                                                                                                                                                                                                               Example 1; SEQ ID NO 7; 224pp; English.
                                                                                                                                                                     Siemers NQ,
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                                           28-MAR-2003; 2003WO-US009676.
                                                                                 28-MAR-2002; 2002US-0368422P.
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                                                                                                                          (BRIM ) BRISTOL-MYERS
                                                                                                                                                                     Feder JN,
                                                                                                                                                                                                              WPI; 2003-804052/75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human; PRO; membrane bound protein; membrane bound receptor; cell proliferation; cell migration; cell differentiation; mitogenic factor; survival factor; optotoxic factor; differentiation factor; neuropeptide; hormone; cell receptor, receptor-ligand interaction; cytostatic; chondrocyte; tumour.
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in the formation, differentiation and maintenance of multicellular corganisms. The fate of many individual cells (for example proliferation, or organisms. The fate of many individual cells (for example proliferation, migration or differentiation) is typically governed by information. Treceived from other cells and the immediate environment. The information is often transmitted by secreted polypeptides (for example mitogenic factors, auryival factors, cytocoxic factors, differentiation factors, neuropeptides and hormones) which are received and interpreted by diverse neuropeptides and hormones) which are received and interpreted by diverse call receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor-ligand interactions. These membrane bound proteins are the interpreted by diverse and proteins, along with the cDNA sequences encoding them. The novel proteins of the invention may have cytostatic activities through the stimulation of chondrocytes. The nucleic actids of the invention may be useful for the manufacture of a medicament for diagnosing or treating etumour in a mammal. In addition, they may be useful for measuring or detecting the expression of a tumour associated gene. The present
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Pred. No. 3e-229;
0; Mismatches 1; Indels
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                                    Claim 10; SEQ ID NO 10; 118pp; English.
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Best Local Similarity 91.5%;
Matches 638; Conservative C
                                                                        invention relates
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The PRO proteins are useful for diagnosing and treating a B cell related disorder, e.g. X-linked infantile hypogammaglobulinemia, polyaacdaride antigen unresponsiveness, selective IgA deficiency, selective IgH deficiency, selective IgA deficiency, selective IgH deficiency with hypogammaglobulinemia of infancy, Burkit's Important hypogammaglobulinemia of infancy, Burkit's Important hypogammaglobulinemia of infancy, Burkit's Important hypogammaglobulinemia of infancy, Burkit's Important hypogammaglobulinemia of infancy, Burkit's Important hypogammaglobulinemia of infancy, Burkit's Important hypogammaglobulinemia of infancy Burkit's Important in hyposacticism, glomerulonephritis, or ansemia, myasthenia gravis, hypoadrencorticism, glomerulonephritis, or anxionament for treating a condition that is responsive to the PRO protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO coding sequences are useful as hybridization probes in chromosome and gene mapping, in preparing PRO proteins, or in generating transgenic animals or knockout animals, which in turn are useful in the development and screening of therapeutically useful reagents.
New PRO polypeptide, useful for diagnosing and treating a B cell related disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
                                                                                                                                                                                                                                                                                Immunosuppressive, Cytostatic, Antiarthritic, Antirheumatic, Antianemic, Antianeric, Antianeric, Antianeric, Antianeric, Muscular, Neuroprotective, Nephrotropic, Antiinflammatory, Gene Therapy, PRO, B cell related disorder, cancer; immune-mediated inflammatory disease, human.
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                                                                             SOEELHYATLNFPGVRPRPBARMPKGTQADYAEVKFQ 697
                                               SQEELHYATLINFPGVRPRPEARMPKGTQADYAEVKFQ
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                                                                                                                                                        ADL82805 standard; protein; 697
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                                                                                                                                                                                                                     (first entry)
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N-PSDB; ADL82804.
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                                                                                                                                                                                                                                                   Human PR071236,
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Wu TD;
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                                                                                                                                                                                                                                                                                                WGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVWVSQANRTVLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            543 VPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPESQE
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                                                                                        ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW
                                                                                                                                                                       181 TGAALSSQGTKPTTSHFSVLSFTPRPQDHNTDLTCHVDFSRKGVSVQRTVRLRVAYAPRD
                                                                                                                                                                                                                LVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP
                                                                                                                                                                                                                                                                                                                                                                                                                NIGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GEFTCHARHPLGSQHVSLSJSVHYSPKLLGPSCSWEAEGLHCSCSSQASPAPSJRWWLGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; sialic acid-binding Ig-related lectin; SIGLEC; asthma; mimune system disease; leuksemia; allergy; inflammatory disease; tissue damage; allergic rhinitis; osteoarthritis; Crohn's disease; psoriasis; rheumatoid arthritis; conjunctivitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sialic acid-binding Ig-related lectin, Siglec-BMS-L3b.
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MILIPLILISSLIGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRODWTGSTPAYGYW MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW

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Best Loca Matches

WPI; 2002-241565/29. N-PSDB; ABK43361 Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein molecules useful for treating immune system diseases such as asthma, leukemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease.

Claim 5; Fig 3B; 209pp; English.

related lectin) protein (31). Pharmaceutical compositions comprising (1) are useful for treating immune system diseases such as asthma, leukaemia or other allegic or inflammatory diseases such as asthma, leukaemia or other allegic or inflammatory diseases. Extracellular domains of (1) represent potential markers for screening, diagnosis, prognosis, follow up assays, and imaging methods. (1) is useful as a target for drugs which inflammatory diseases such as allergic rhinitis, osteoarthritis, Crohn's disease, psoriasis, rheumatoid arthritis, conjunctivitis, etc. (1) is also useful for monitoring the course of disease or disorders, and for identifying agents that bind with and/or modulate the biological activity of SIGLEC-BMS proteins. The nucleic acid molecules (11) encoding (1) are useful in diagnosis and/or prognosis methods, and to detect the presence useful in diagnosis and/or broughous (11) are useful as nucleic acid probes proteins in a biological sample. (11) are useful as nucleic acid probes are useful for screening genomic library to isolate a genomic clone of SIGLEC gene. SIGLEC-BMS gene copy number is determined for detecting diseases or disorders associated with SIGLEC-BMS transcripts or proteins. The SIGLEC-BMS antiodies are also used to detect, sont or isolate estimated semined semined for detecting diseases or disorders associated with SIGLEC-BMS transcripts or proteins. The SIGLEC-BMS antiodies are also used to detect, sont or isolate estimated expressing signated-BMS proteins and in diagnostic imaging technology.

ADUSTOR ADUSTOR PERPENSION NUMBER SIGLEC-BMS and the detecting and in diagnostic imaging technology. The invention relates to an isolated SIGLEC (sialic acid-binding Ig-NY XX WPT; 2002-241

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Seguence 622 AA;

0 Gaps ٠, 97.7%; Score 3299; DB 5; Length 622; 100.0%; Pred. No. 8.1e-227; ive 0; Mismatches 0; Indels ( 622; Conservative Query Match Best Local Similarity Matches 622; Conserv

78 OSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRVERGSYVRYNFMNDGFFL 137

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240 181 OPOGNVPYLEAQKGOFLRLLCAADSOPPATLSWVLONRVLSSSHPWGPRPLGLELPGVKA QPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHPWGPRPLGLELPGVKA

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241 GDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVWVSQANRTVLENGNGTSLPVLEGQS 258 GDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLENLGNGTSLPVLEGQS LCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQH 318

377

361 VSLSLSVHYSPKILGPSCSWEAEGLHCSCSSQASPAPSLRWWLGBELLEGNSSQDSFEVT 420 378 VSLSLSVHYSPKLLGPSCSWEAEGLHCSCSSQASPAPSLRWWLGEELLEGNSSQDSFEVT

> 7 - 음 ò

301 LCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQH

438 PSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQSGSILQLPDKKGLISTAFSNGAFLG

498 IGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNQKA 557

600 TPNSPRTPLPPGAPSPESKKNOKKOYQLPSFPEPKSSTQAPESQESCHYATLNFPGV 541 TPNSPRTPLPPGAPSPESKKNOKKOYOLPSPPEPKSSTQAPESOESQEELHYATLNFPGV 639 601 RPRPEARMPKGTQADYAEVKFQ RPRPEARMPKGTQADYAEVKFQ 558 ઠ g ò g

ADD19314 standard; protein; 710 AA.

15-JAN-2004 (first entry)

Human secreted protein from gene 18 #3.

human secreted protein, cytostatic, antibacterial, virucide, neuroprotective, gynaecological, gastrointestinal-Gen, cardiont cardiovascular-Gen, emphrotropic, antiinflammatory, muscular-Gen, respiratory-Gen, immunosuperssive, cerebroprotective, vasotropic, nootropic, antiallergic, cancer, bacterial infection, viral infection, muscular disorder; immune system disorder; blood disorder; muscular disorder; cardiovascular disorder; cardiovascular disorder; cardiovascular disorder; renal disorder; inflammatory disorder; proliferative disorder; human

Homo sapiens

WO2003052377-A2 

26-JUN-2003

06-NOV-2002; 2002WO-US035606

07-NOV-2001; 2001US-0331046P.

(HUMA-) HUMAN GENOME SCI INC

Rosen CA, Ruben SM;

WPI: 2003-533050/50. N-PSDB; ADD19239 New isolated nucleic acids encoding signal transduction pathway component polypeptides, useful for diagnosing, treating, and/or preventing disorders, such as cancer, infections, cardiovascular and inflammatory diseases

Claim 11; SEQ ID NO 141; 554pp; English

The invention relates to an isolated nucleic acid molecule (CDNA)

concoding a human secreted protein, representing one of 85 novel genes.

Also included are recombinant vectors, host cells (expressing the protein), the secreted proteins (including their fragments, epitopes and homologues), an isolated antibody that binds specifically to the protein, diagnosing a pathological condition or susceptibility to a pathological condition (comprising determining the presence or absence of a mutation in the nucleic acid and diagnosing a condition based on the presence or absence or a susceptibility to a pathological condition (comprising determining the protein in a biological condition or susceptibility to a pathological condition (comprising determining the presence or amount of expression of the protein in a biological sample or and angenosing a condition based on the presence or amount of expression of the protein in a biological condition by administering the nucleic acid or protein to a mammalian subject, by administering the nucleic acid or protein, the gene corresponding to the cDNA sequence, and identifying an activity in a biological assay (comprising expressing the nucleic acid in a cell, isolating the

Human, sialic acid-binding Ig-related lectin; SIGLEC; asthma; mimune system disease; leukaemia; allergy; inflammatory disease; tissue damage; allergic rhinitis; osteoarthritis; Crohn's disease; psoriasis; rheumatoid arthritis; conjunctivitis.

Whitney G; 8

Chang H,

Longphre M,

(BRIM ) BRISTOL-MYERS

20-JUL-2001; 2001WO-US023082 21-JUL-2000; 2000US-0220139P

WO200208257-A2 Homo sapiens.

31-JAN-2002

Sialic acid-binding Ig-related lectin, Siglec-BMS-L3a.

(first entry)

05-JUN-2002

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supernatant, detecting an activity in a biological assay and identifying the protein in the supernatant having the activity). The nucleic acids and proteins display the following activities Cytostatic, antibacterial, Virucide, Neuroprotective, Gynaecological, Gastrointestinal-Gen, Cardiant, Cardiavascular-Gen, Nephrotropic, Antinflammatory, Muscular-Gen, Respiratory Cen, Immunosuppressive, Carebroprotective, Vasotropic, Nootropic, Antialiergic. The methods and compositions of the present invention are useful for diagnoshing, treating, preventing and/or prognosticating disorders related to the novel polypeptides, such as cancer, bacterial or viral infections, and neural, immune system, blood, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, remal, inflammatory or proliferative disorders (many examples of these diseases and disorders are given in the specification). The present sequence represents a novel secreted protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 7; Length 710;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 3174.5; DB 7;
Pred. No. 7.6e-218;
2; Mismatches 9;
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The invention relates to an isolated SIGLEC (sialic acid-binding Igrelated lectin) protein (I). Pharmaceutical compositions comprising (I) are unseful for treating immune system diseases such as asthma, leukaemia or other allergic or inflammatory diseases such as asthma, leukaemia or other allergic or inflammatory diseases. Extracellular domains of (I) represent potential markers for screening, diagnosis, prognosis, following passays, and imaging methods. (I) is useful as a traget for drugs which inhibit inflammation, tissue damage and remodeling in asthma, and inflammatory diseases such as allergic rhinitis, osteoarthritis, Crohn's disease, psoriasis, rheumatorid arthritis, conjunctivitis, erc. (I) is also useful for monitoring the course of disease or disorders, and for identifying agents that bind with and/or modulate the biological activity or SIGLEC-BMS proteins. The nucleic acid molecules (II) encoding (I) are useful in diagnosis and/or prognosis methods, and to detect the presence and/or amount of SIGLEC-BMS nucleotide sequences and/or SIGLEC-BMS proteins in a biological sample. (II) are useful as nucleic acid probes proteins in a biological sample. (II) are useful as nucleic acid probes diseases or disorders associated with SIGLEC-BMS transcripts or proteins. The SIGLEC-BMS antibodies are also used to detect, sort or isolate cells expressing SIGLEC-BMS proteins and in diagnostic imaging technology.

ANUBLOTA-ANUBROSS represent human SIGLEC amino acid sequences of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein molecules useful for treating immune system diseases such as asthma, leukemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease.
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llarity 85.1%; Pred. No. 1.7e-191;
Conservative 0; Mismatches 0;
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N-PSDB; ABK43360.
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AAU87074 standard; protein; 544 AA

RESULT 13 AAU87074 ID AAU87

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98US-0079523P

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506 QESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ 544

RESULT 15 AAB44280

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The present invention describes secreted and transmembrane polypeptides and their polymucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AAZ3381 to AAZ34338, and AAX41685 to AAX41774 represent polymucleotide and polypeptide sequence given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FKAVTETTKGAPVATNHOSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTV 300
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                                                                                                                                                secreted and transmembrane polypeptides and their polynucleotides, tul for treating blood coagulation disorders, cancers and cellular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95;
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84.8%; Pred. No. 1.4e-190;
live 0; Mismatches 2; Indels 95;
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                                                     Baker
                                                     Yuan J,
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                                                       Gurney A,
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tches 542; Conservative
               GETH ) GENENTECH INC.
                                                                                        WPI; 1999-551358/46
                                                                                                                                                               useful for treating adhesion disorders.
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AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bicactive molecules to cells and for modulating biclogical activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide provide specific targeting of bicactive molecules to cells. AAC786700 to AAC78887 represent PCR primers and probes used in the isolation of the PRO polynucleotide sequences
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    Gerritsen ME;
    Hillan KJ;
    Roy MA, Shelton

                                                                                                 Human, secreted protein; transmembrane protein, PRO, BST; cytostatic, expressed sequence tag; detection; cancer.
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                                                                            Human PRO940 (UNQ477) protein sequence SEQ ID NO:259
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AAB44280 standard; protein; 544
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99US-0123957P.
99US-012673P.
99US-0131445P.
99US-0134287P.
99US-0141037P.
99US-0141037P.
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99WO-US028565
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Filvaroff E,
Godowski PJ,
Kuo SS, Napi,
Tumas D, Wil
                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC.
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N-PSDB; AAC78510.
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30-DEC-1999;
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28-APR-1999;
14-MAY-1999;
26-JUL-1999;
26-JUL-1999;
30-NOY-1999;
02-DEC-1999;
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12-MAR-1999;
29-MAR-1999;
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Goddard A,
Kljavin IJ,
Stewart TA,
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540 445 900 505

NVVPTAGPLAQKRNQKATPNSPRTPPPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPES

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QESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ 639

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                                                                                                                                 1 MILPLILSSILGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRODWIGSTPAYGYW
Query Match 82.6%; Score 2790.5; DB 3; Length 544;
Best Local Similarity 84.8%; Pred. No. 1.4e-190;
Matches 542; Conservative 0; Mismatches 2; Indels 95; Gaps
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Search completed: November 5, 2004, 13:53:24 Job time: 76.3927 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

protein search, using sw model protein Θ

5, 2004, 13:50:17; Search time 74.3927 Seconds (without alignments) 3081.324 Million cell updates/sec November Run on:

Title: Perfect score:

US-09-937-636-4 3377 1 MLDPLLLSSLIAGGSQAMDGR......RPEARMPKGTQADYAEVKFQ 639

Sequence:

Scoring table:

2002273 seqs, 358729299 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp1980s:*
geneseqp1990s:*
geneseqp2000s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

AAW81023 RESULT

AAW81023 standard; protein; 639 AA

AAW81023;

(first entry) 26-APR-1999 Human sialoadhesin family 4 (SAF-1) polypeptide.

SAF-4; sialoadhesin family, human, therapy, diagnosis; cancer; inflammation, autoimmune disease; allergy; asthma; inflammation; cerebellar degeneration; Alzheimer's disease; Parkinson's disease; multiple sclerosis, amyotrophic lateral sclerosis; head injury; septic shock; sepsis; stroke; osteoporosis; osteoarthritis; ischemia repertusion injury; cardiovascular disease; kidney disease; liver disease; myocardial infarction; hypotension; hypertension; AIDS; myelodysplastic syndrome; aplastic anaemia; baldness; infection. 

Homo sapiens.

WO9853840-A1. 03-DEC-1998.

98WO-US010791. 27-MAY-1998; (SMIK ) SMITHKLINE BEECHAM CORP.

97US-0047572P.

27-MAY-1997;

Kikly KK, Erickson-Miller CL;

WPI; 1999-080779/07. N-PSDB; AAV99911.

t C New sialoadhesin family 4 polypetides and polynucleotides - useful treat various diseases associated with SAF-4 expression.

Claim 1; Page 31; 48pp; English.

This is the amino acid sequence of new human sialoadhesin family 4 (SAF-4), as deduced from the nucleotide sequence of an isolated cDNA clone (see AAV99911). SAF-4 polynucleotides and polypeptides, and methods for producing such polypeptides in transformed host cells using recombinant techniques are disclosed. SAF-4, its agonists and antagonists, and nucleic acid molecules that enhance or inhibit SAF-4 expression, may be used to treat patients in need of enhancement or inhibition of SAF-4

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include cancer, inflammation, autoimmunity, allergy, asthma, treatment arthritis, CNS inflammation, cerebellar degeneration, Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, head injury damage and other neurological disorders, septic shock, sepsis, stroke, osteoporosis, osteoarthritis, ischemia reperfusion injury, cardiovascular disease, Midney disease, liver disease, ischemic injury, myocardial infarction, hypotension, hypertension, AlDS, myelodysphastic syndromes and other haematologic abnormalities, aplastic infections related to SAF-4 polypeptide activity. Methods of identifying agonists, antagonists, inhibitors are also provided, as well as diagnostic assays for detecting diseases associated with inappropriate SAF-4 activity or levels
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ID AAY97543 standard, protein, 639
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(first entry)

12-FEB-2001

AAY97543;

This sequence is a human obesity protein binding protein-2 homologue (hobbensh) of the invention. The hOB-BP2h nucleic acids and polypeptides may be used for the manufacture of a medicament for the treatment of obesity and/or obesity-related disorders. The hOB-BP2h nucleic acids are useful as probes or amplification primers in the detection, quantification or isolation of gene sequences or transcripts, for recombinant expression of hOB-BP2h polypeptides, as immunogens in the preparation and screening of antibodies, and in sense or antisense suppression of one or more hOB-BP2h antibodies, and in sense or antisense suppression of one or more hOB-BP2h antigenic epitope-bearing peptides and polypeptides are useful for raising or screening antibodies that specifically binds to the hOB-BP2h 241 HPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTV 300 420 BRGSYVRYNFMNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAP FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV Human obesity protein binding protein-2 homologue; hOB-BP2h; obesity; obesity, obesity.related disorder; therapy. HPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTV MILPLILISSILIGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW **ERGSYVRYNFMNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAP** RDLVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSS 1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW RDLVISISRDNTPALBPQPQGNVPYLBAQKGQFLRILCAADSQPPATLSWVLQNRVLSSS LENLGNGTSLPVLEGGSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVE HEGEFTCHARHPLGSQHVSLSLSVHYSPKLLGPSCSWEAEGLHCSCSSQASPAPSLRWWL FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV nucleic acids, medicament for Gaps .; 0 639 Length Indels New human obesity protein binding protein-2 homologue polynucleotides and polypeptides useful for producing treating obesity and/or obesity-related disorders. Human obesity protein binding protein-2 homologue #2 100.0%; Score 3377; DB 3; 100.0%; Pred. No. 2.3e-232; ive 0; Mismatches 0; Claim 9; Page 89-91; 92pp; English 22-MAR-2000; 2000WO-US006682; 99US-0127667P al Similarity 100. 639; Conservative (ELIL ) LILLY & CO ELI WPI; 2000-664992/64. N-PSDB; AAA37848 Sequence 639 AA; WO200059942-A2 Wei J; Homo sapiens, 02-APR-1999; polypeptides Query Match Best Local S: Matches 639 61 61 121 121 181 181 301 301 361 Su EW, d g à ò à g à 업 ò ద ò 원 à

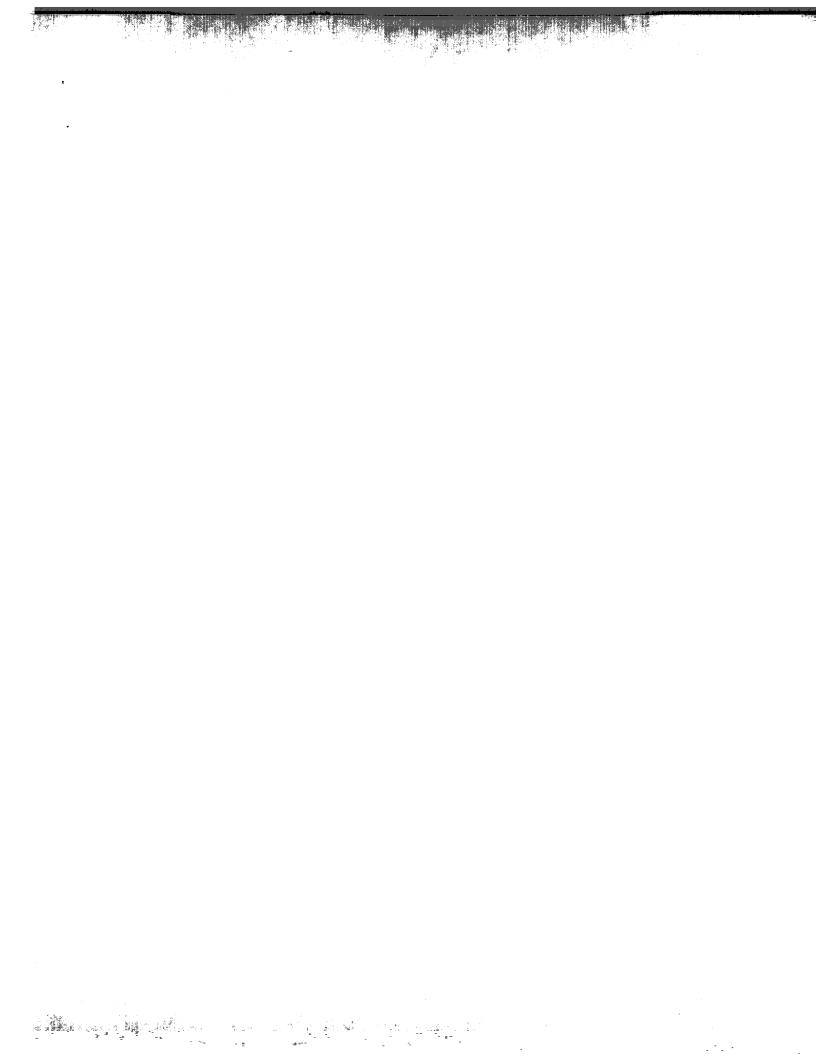
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Human sialoadhesin family 4 (SAF-1) related EST clone.

SAF-4; sialoadhesin family; human; therapy; diagnosis; cancer; inflammation; autoimmune disease; allergy; asthma; inflammation; cerebellar degeneration; Alzheimer's disease; Parkinson's disease; multiple sclerosis, amyotrophic lateral sclerosis; head injury; septic shock; sepsis; stroke; osteoporosis; osteoarthritis; ischemia reperfusion injury; cardiovascular disease; Kidney disease; liver disease; myocardial infarction; hypotension; hypertension; AlDS; myelodysplastic syndrome; aplastic anaemia; baldness; infection; se.

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New sialoadhesin family 4 polypetides and polynucleotides - useful to treat various diseases associated with SAF-4 expression.

Claim 13; Page 31-32; 48pp; English.

This is the nucleotide sequence of an expressed sequence tag (EST) clone that encodes a polypeptide (see AAM81024) which shows close homology and/or structural similarity (e.g. a conservative amino acid difference) to new human similarity (e.g. a conservative amino acid difference) conew human similarity (e.g. a conservative amino acid difference) conew human similarity (e.g. a conservative amino acid difference) collypeptides in transformed host cells using recombinant techniques, are disclosed. SAF-4, its agonists and antagonists, and nucleic acid antagonists, and nucleic acid molecules that enhancement or inhibit taff-4 expression, may be used to treat patients in need of enhancement or inhibit to SAF-4 expression or activity. Conditions that may benefit from such treatment include cancer, inflammation, cerebellar degeneration, Alzehimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, head injury campage and other neurological disorders, septic shock, sepsis, stroke, osteoporosis, osteobarthritis, ischemia reperfusion injury, myocardial inflammation, hypotension, historians, myelodysplastic synder, osteoporosis, osteobarthritis, ischemia reperfusion injury, myocardial inflamentologic abnormalities, aplastic anaemia, male baldness and other haematologic abnormalities, aplastic anaemia, male baldness pattern and bacterial, protozoal, fungal and viral infections related to she hat belypeptide activity. Methods of identifying agonists, says, and the pattern and seases associated with inappropriate SAF-4 activity or anaemia. 

Sequence 3099 BP; 770 A; 907 C; 813 G; 607 T; 0 U; 2 Other;

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1071 CTGAGCCCTCCCAGCCCTCAGACCCCGGGGTCCTGGAGCTGCTCGGGGTTCAAGTGGAG 1130
                                                                           1141 AGCCTCTCCGTGCACTACTCCCCGAAGCTGCTGGGCCCCTTCTGGTGGGAGGCTGAG 1200
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Human sialoadhesin family 4 (SAF-1) cDNA.
                 AAV99911 standard; cDNA; 3099 BP.
                                                       (first entry)
                                    AAV99911;
RESULT 3
AAV99911
                  0 x 2 x 5 x 5 x 5 x 5 x 5
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SAF-4; sialoadhesin family; human; therapy; diagnosis; cancer; inflammation; autoimmune disease; allergy; asthma; inflammation; cerebellar degeneration; Alzheimer's disease; Parkinson's disease;

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This cDNA clone codes for new human stalcadhesin family 4 (SAF-4)
polypeptide (See AAM81023). It can be obtained e.g. from a CDNA library
carived from mRNA in cells of human primary dendritic cells, using
expressed sequence tag analysis. SAP-4 polymocleotides and polypeptides
and methods for producing such polypeptides by recombinant techniques are
and methods for producing such polypeptides by and mucleic acid
molecules that enhance or inhibit SAF-4 expression, may be used to treat
patients in need of enhancement or inhibition of SAF-4 expression or
cativity. Conditions that may benefit from such treatment include cancer,
inflammation, autoimmunity, allergy, acthma, rheumatoid arthits. CNS
inflammation, cerebellar degeneration, Alzheimer's disease, harkinson's
disease, multiple solerosis, amyortophic lateral sclerosis, head injury
damage and other neurological disorders, septics shock, sepsis, stroke,
disease, kidney disease, liver disease, ischemic injury, cardiovascular
disease, kidney disease, liver disease, ischemic injury, wycardial
infartion, hypotension, hypettension, AlDS, myclodysplastic syndromes
and other haematologic abnormalities, aplastic anaemia, male baldness
catern and bacterial, protozoal, fungal and viral infections related to
sactern and bacterial, protozoal, fungal and viral infections related
categonists/inhibitors are also provided, as well as diagnostic assays
for detecting diseases associated with inappropriate SAF-4 activity or 230 121 TGCTCTTTCTCCTACCCCCGACAAGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGG 180 TTCTGGATACGAGTGCAGGAGTCAGTGATGGTGCCGGAGGGCCTGTGCATCTCTGTGCCC 120 septic shock, sepsis, stroke, osteoporosis, osteoarthritis, ischemia reperfusion injury; cardiovascular disease, kidney disease, liver disease, myocardial infarction; hypotension; hypertension, AIDS, myelodysplastic syndrome, aplastic anaemia, baldness, infection; ss. 111 TGCTCTTTCTCCTACCCCCGACAGACTGGACAGGGTCTACCCCCAGCTTATGGCTATGG New sialcadhesin family 4 polypetides and polynucleotides - useful to treat various diseases associated with SAF-4 expression. 0; Gaps multiple sclerosis, amyotrophic lateral sclerosis; head injury; 100.0%; Score 1917; DB 2; Length 3099; 100.0%; Pred. No. 0; ive 0; Mismatches 0; Indels 0; Sequence 3099 BP; 769 A; 908 C; 813 G; 607 T; 0 U; 2 Other; Location/Qualifiers 51. .1970 Claim 2; Page 30-31; 48pp; English. (SMIK ) SMITHKLINE BEECHAM CORP. Kikly KK, Erickson-Miller CL; 97US-0047572P. 98WO-US010791 Best Local Similarity 100.0 Matches 1917; Conservative /*tag= a 1999-080779/07. P-PSDB; AAW81023 Homo sapiens. WO9853840-A1. 27-MAY-1998; 27-MAY-1997; 03-DEC-1998 61 Query Match evels g ò g 쥠 ò

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